



# STIC Search Report

## Biotech-Chem Library

Rapm Rapm

STIC Database Tracking Number: 110859

TO: Georgia L Helmer  
Location: CM1/9B12/9D14  
Art Unit: 1638  
Tuesday, December 23, 2003

Case Serial Number: 09/289346

From: Edward Hart  
Location: Biotech-Chem Library  
CM1-6B02  
Phone: 305-9203

edward.hart@uspto.gov

### Search Notes

Examiner Helmer,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

An pending  
files  
Removed  
Dec 23, 2003

# 10 - OK  
2 tie  
3  
4  
5  
6

7  
8  
9  
-

Hart, Edward

110859

**From:** STIC-Biotech/ChemLib  
**Sent:** Tuesday, December 23, 2003 8:47 AM  
**To:** Hart, Edward  
**Subject:** FW: Rush seq search--US09/289,346

-----Original Message-----

**From:** Chan, Christina  
**Sent:** Tuesday, December 23, 2003 7:59 AM  
**To:** Helmer, Georgia; STIC-Biotech/ChemLib  
**Subject:** RE: Rush seq search--US09/289,346

Please rush. Thanks Chris

*Chris Chan*

TC 1600 New Hire Training Coordinator and SPE 1644  
308-3973  
CM-1, 9B19

-----Original Message-----

**From:** Helmer, Georgia  
**Sent:** Monday, December 22, 2003 3:16 PM  
**To:** Chan, Christina  
**Subject:** Rush seq search--US09/289,346

Could you please do a sequence search of SEQ ID Nos 2-10 of case US 09/289,346.

Thanks in advance!

Georgia Helmer PhD  
Patent Examiner - art unit 1638  
(703) 308-7023  
CM1 - 9D14  
mailbox 9312

After 6 January 2004,  
Phone (571) 272-0796  
Office: Remson 2C15

12/23/03  
ABSSP  
9-AA



# STIC SEARCH RESULTS

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact

Mary Hale, Information Branch Supervisor  
308-4258, CM1-1E01

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art found, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not** found:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 - Circ. Desk



Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

***Because they contain data that is confidential, the results of Pending database searches should not be left in the case .***



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds  
(without alignments)  
340.128 Million cell updates/sec

Title: US-09-289-346B-10  
Perfect score: 364  
Sequence: 1 TLVGFQVDSRGSCQT.....FQFHLNLSNLDRIFDKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	364	100.0	70	21	AA198686
2	349	95.9	70	21	AA198677
3	349	95.9	356	21	AA198687
4	341	93.7	70	21	AA198685
5	338	92.9	70	21	AA198688
6	337	92.6	70	21	AA198692
7	335	92.0	70	21	AA198684
8	335	92.0	70	21	AA198690
9	334	91.8	70	21	AA198678
					Mutant peptide der
					Peptide fragment f
					Amino acid sequenc
					Mutant peptide der
					Mutant peptide der
					Mutant peptide der
					Mutant peptide der
					Mutant peptide der

10	333	91.5	70	21	AA198689
11	331	90.9	70	21	AA198680
12	331	90.9	70	21	AA198691
13	328	90.1	70	21	AA198681
14	327	89.8	70	21	AA198683
15	325	89.3	70	21	AA198682
16	317	87.1	70	21	AA198679
17	223	61.3	353	18	AAW34338
18	223	61.3	353	18	AAW34332
19	223	61.3	353	18	AAW34333
20	223	61.3	353	18	AAW34334
21	223	61.3	353	18	AAW34335
22	221	60.7	353	8	AAF70407
23	221	60.7	359	17	AAW34326
24	221	60.7	359	17	AAW34325
25	221	60.7	359	17	AAW34324
26	221	60.7	361	18	AAW34323
27	221	60.7	361	18	AAW34322
28	221	60.7	361	18	AAW34321
29	212.5	58.4	361	18	AAW34320
30	208.5	57.3	50	23	AAO22043
31	207	56.9	362	19	AAW56495
32	206	56.6	357	18	AAW34329
33	206	56.6	357	18	AAW34330
34	206	56.6	357	18	AAW34331
35	198	54.4	357	18	AAW34337
36	198	54.4	142	24	ABP58120
37	95	26.1	857	23	ABP62804
38	68	18.7	945	22	ABW65231
39	65.5	18.0	945	22	ABW65231
40	65	17.9	292	21	AAV92317
41	65	17.9	335	21	AAV92318
42	64.5	17.7	685	22	ABW70391
43	64	17.6	712	23	AAU82975
44	64	17.6	722	23	ABP73316
45	63.5	17.4	163	21	AAW60400

ALIGNMENTS

RESULT 1

AA198686

ID AA198686 standard; peptide; 70 AA.

AC AA198686;

XX 22-JAN-2001 (first entry)

DT Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

DE Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

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XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

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XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX Geminivirus; replication protein; Rep protein; All; transgenic plant;

XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 PA Hanley-Bowdoin L, Orozco BM, Kong L;  
 PI WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX  
 XX Claim 53; Page 46; 73pp; English.  
 XX The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;  
 Query Match 100.0%; Score 364; DB 21; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-38;  
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
 DB 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 2  
 AAB18677  
 ID AAB18677 standard; peptide; 70 AA.  
 XX AAB18677;  
 XX 22-JAN-2001 (first entry)  
 XX Peptide fragment from Rep protein of TGMV (amino acids 110-179).  
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX Tomato golden mosaic virus.  
 OS WO200054573-A1.  
 PN 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 PF 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 PA Hanley-Bowdoin L, Orozco BM, Kong L;  
 PI WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX  
 XX Disclosure; Page 18; 73pp; English.  
 XX The present sequence is derived from a geminivirus replication (Rep)  
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,  
 CC catalyzes cleavage and ligation of single-stranded DNA, and interacts  
 CC with other viral and host proteins. Mutants of the AL1 protein are used  
 CC to produce transgenic plants. The mutation in AL1 is present in a  
 CC ribosome binding region, and expression of mutant AL1 protein imparts  
 CC increased resistance to geminivirus infection in the plant. Mutant AL1  
 CC proteins are useful for producing plants having increased resistance or  
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,  
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl  
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato  
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,  
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or  
 CC beet curly top virus.  
 XX  
 SQ Sequence 70 AA;  
 Query Match 95.9%; Score 349; DB 21; Length 70;  
 Best Local Similarity 95.7%; Pred. No. 1.3e-36;  
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
 DB 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 3  
 AAB18687  
 ID AAB18687 standard; peptide; 356 AA.  
 XX AAB18687;  
 XX 22-JAN-2001 (first entry)  
 XX Amino acid sequence of a geminivirus replication protein of TGMV.  
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX Tomato golden mosaic virus.  
 OS Key Location/Qualifiers  
 FH Misc-difference 354 /note= "unspecified amino acid"  
 FT WO200054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 PF 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 PA Hanley-Bowdoin L, Orozco BM, Kong L;  
 PI WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence  
PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
PT -  
XX  
PS Disclosure; Page 47-48; 73pp; English.  
XX  
CC The present sequence represents a geminivirus replication (Rep)  
CC protein, which is also known as AL1. AL1 binds double-stranded DNA,  
CC catalyses cleavage and ligation of single-stranded DNA, and interacts  
CC with other viral and host proteins. Mutants of the AL1 protein are used  
CC to produce transgenic plants. The mutation in AL1 is present in a  
CC ribosome binding region, and expression of mutant AL1 protein imparts  
CC increased resistance to geminivirus infection in the plant. Mutant AL1  
CC proteins are useful for producing plants having increased resistance or  
CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,  
CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl  
CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato  
CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,  
CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or  
XX beet curly top virus.  
XX  
SQ Sequence 356 AA;  
Query Match 95.9%; Score 349; DB 21; Length 356;  
Best Local Similarity 95.7%; Pred. No. 1e-35; Indels 0; Gaps 0;  
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TLVWGFEVDGRSARGCGQTSNDLLLEALNASSKEEALQIRKEIKPEKYLFOFHNLSNL 60  
DB 110 TLVWGFEVDGRSARGCGQTSNDAAEALNASSKEEALQIRKEIKPEKYLFOFHNLSNL 169  
QY 61 DRIFDKTPEP 70  
DB 170 DRIFDKTPEP 179  
RESULT 4  
AAB18685  
ID AAB18685 standard; peptide; 70 AA.  
AC AAB18685;  
XX  
XX 22-JAN-2001 (first entry)  
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
XX ribosome binding region; resistance; geminivirus infection.  
XX Synthetic.  
XX Tomato golden mosaic virus.  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 10 /note= "wild type residue replaced with Ala"  
FT Misc-difference 10 /note= "wild type residue replaced with Ala"  
XX  
XX WO200054573-A1.  
XX  
XX 21-SEP-2000.  
XX  
XX 15-MAR-2000; 2000WO-US06759.  
XX  
XX 18-MAR-1999; 99US-0125004.  
XX 09-APR-1999; 99US-0289346.  
XX  
XX (UYN-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hanley-Bowdoin L, Orozco BM, Kong L;  
XX WPI; 2000-618851/59.  
XX  
XX Transgenic plants with increased resistance to geminivirus infection  
XX comprise a nucleic acid construct containing a nucleic acid sequence

PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
PT -  
XX  
PS Claim 53; Page 46; 73pp; English.  
XX  
CC The present sequence represents a mutant peptide, derived from a  
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
CC protein are used to produce transgenic plants. The mutation in AL1 is  
CC present in a ribosome binding region, and expression of mutant AL1  
CC protein imparts increased resistance to geminivirus infection in the  
CC plant. Mutant AL1 proteins are useful for producing plants having  
CC increased resistance or reduced sensitivity to a geminivirus such as  
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
CC virus, cotton leaf curl virus or beet curly top virus.  
XX  
XX Sequence 70 AA;  
Query Match 93.7%; Score 341; DB 21; Length 70;  
Best Local Similarity 94.3%; Pred. No. 1.3e-35;  
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 TLVWGFEVDGRSARGCGQTSNDLLLEALNASSKEEALQIRKEIKPEKYLFOFHNLSNL 60  
DB 1 TLVWGFEVDGRSARGCGQTSNDAAEALNASSKEEALQIRKEIKPEKYLFOFHNLSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70  
RESULT 5  
AAB18688  
ID AAB18688 standard; peptide; 70 AA.  
XX  
XX AAB18688;  
XX  
XX 22-JAN-2001 (first entry)  
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
XX ribosome binding region; resistance; geminivirus infection.  
XX Synthetic.  
XX Tomato golden mosaic virus.  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 19 /note= "wild type residue replaced with Ala"  
FT Misc-difference 20 /note= "wild type residue replaced with Ala"  
XX  
XX WO200054573-A1.  
XX  
XX 21-SEP-2000.  
XX  
XX 15-MAR-2000; 2000WO-US06759.  
XX  
XX 18-MAR-1999; 99US-0125004.  
XX 09-APR-1999; 99US-0289346.  
XX  
XX (UYN-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hanley-Bowdoin L, Orozco BM, Kong L;  
XX WPI; 2000-618851/59.  
XX  
XX Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence  
PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
XX  
XX  
XX  
XX Disclosure; Page 48; 73pp; English.  
XX  
XX The present sequence represents a mutant peptide, derived from a  
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
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CC plant. Mutant AL1 proteins are useful for producing plants having  
CC increased resistance or reduced sensitivity to a geminivirus such as  
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
CC virus, cotton leaf curl virus or beet curly top virus.  
XX  
XX Sequence 70 AA;  
SQ  
Query Match 92.9%; Score 338; DB 21; Length 70;  
Best Local Similarity 92.9%; Pred. No. 3.2e-35;  
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 TLWGFQVDGRSARGCCTSDLLLEALNASSKEALQIIRKIPKYLQFPHNLSNL 60  
DB 1 TLWGFQVDGRSARGCCTSDAAAEALNASSKEALQIIRKIPKYLQFPHNLSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70  
RESULT 6  
AAB18692  
ID AAB18692 standard; peptide; 70 AA.  
XX  
XX AAB18692;  
XX  
XX 22-JAN-2001 (first entry)  
XX  
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
XX  
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
XX ribosome binding region; resistance; geminivirus infection.  
XX  
XX Synthetic.  
XX Tomato golden mosaic virus.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 66 /note= "wild type residue replaced with Ala"  
FT Misc-difference 69 /note= "wild type residue replaced with Ala"  
FT  
FT  
FT  
XX WO200054573-A1.  
XX  
XX 21-SEP-2000.  
XX  
XX 15-MAR-2000; 2000WO-US06759.  
XX  
XX 18-MAR-1999; 99US-0125004.  
XX 09-APR-1999; 99US-0289346.  
XX  
XX (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hanley-Bowdoin L, Orozco BM, Kong L;  
XX WPI; 2000-618851/59.  
XX

PT Transgenic plants with increased resistance to geminivirus infection  
PT comprise a nucleic acid construct containing a nucleic acid sequence  
PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
XX  
XX  
XX Disclosure; Page 50; 73pp; English.  
XX  
XX The present sequence represents a mutant peptide, derived from a  
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CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
CC protein are used to produce transgenic plants. The mutation in AL1 is  
CC present in a ribosome binding region, and expression of mutant AL1  
CC protein imparts increased resistance to geminivirus infection in the  
CC plant. Mutant AL1 proteins are useful for producing plants having  
CC increased resistance or reduced sensitivity to a geminivirus such as  
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
CC virus, cotton leaf curl virus or beet curly top virus.  
XX  
XX Sequence 70 AA;  
SQ  
Query Match 92.6%; Score 337; DB 21; Length 70;  
Best Local Similarity 92.9%; Pred. No. 4.3e-35;  
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 TLWGFQVDGRSARGCCTSDLLLEALNASSKEALQIIRKIPKYLQFPHNLSNL 60  
DB 1 TLWGFQVDGRSARGCCTSDAAAEALNASSKEALQIIRKIPKYLQFPHNLSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70  
RESULT 7  
AAB18684  
ID AAB18684 standard; peptide; 70 AA.  
XX  
XX AAB18684;  
XX  
XX 22-JAN-2001 (first entry)  
XX  
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
XX  
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
XX ribosome binding region; resistance; geminivirus infection.  
XX  
XX Synthetic.  
XX Tomato golden mosaic virus.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 7 /note= "wild type residue replaced with Ala"  
FT Misc-difference 8 /note= "wild type residue replaced with Ala"  
FT  
FT  
FT  
XX WO200054573-A1.  
XX  
XX 21-SEP-2000.  
XX  
XX 15-MAR-2000; 2000WO-US06759.  
XX  
XX 18-MAR-1999; 99US-0125004.  
XX 09-APR-1999; 99US-0289346.  
XX  
XX (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hanley-Bowdoin L, Orozco BM, Kong L;  
XX WPI; 2000-618851/59.  
XX

XX Transgenic plants with increased resistance to geminivirus infection  
PT comprise a nucleic acid construct containing a nucleic acid sequence  
PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
PT -  
XX  
XX  
PS Claim 52; Page 45; 73pp; English.  
XX  
XX The present sequence represents a mutant peptide, derived from a  
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
CC protein are used to produce transgenic plants. The mutation in AL1 is  
CC present in a ribosome binding region, and expression of mutant AL1  
CC protein imparts increased resistance to geminivirus infection in the  
CC plant. Mutant AL1 proteins are useful for producing plants having  
CC increased resistance or reduced sensitivity to a geminivirus such as  
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
CC virus, cotton leaf curl virus or beet curly top virus.  
XX  
SQ Sequence 70 AA;  
Query Match 92.0%; Score 335; DB 21; Length 70;  
Best Local Similarity 92.9%; Pred. No. 7.8e-35;  
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFPQHNLNSNL 60  
DB 1 TLVWGEAAVDGSRARGGCGTSDNDAALNASSKEEALQIIREKIPEKYLFPQHNLNSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70  
RESULT 8  
AAB18690  
ID AAB18690 standard; peptide; 70 AA.  
XX  
AC AAB18690;  
XX  
DT 22-JAN-2001 (first entry)  
XX  
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
XX  
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
KW ribosome binding region; resistance; geminivirus infection.  
XX  
OS Synthetic.  
OS Tomato golden mosaic virus.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 27 /note= "wild type residue replaced with Ala"  
FT Misc-difference 30 /note= "wild type residue replaced with Ala"  
FT  
XX  
PN WO2000054573-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 15-MAR-2000; 2000WO-US06759.  
XX  
PR 18-MAR-1999; 99US-0125004.  
PR 09-APR-1999; 99US-0289346.  
XX  
XX (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
PI Hanley-Bowdoin L, Orozco BM, Kong L;  
XX

DR WPI; 2000-618851/59.  
XX Transgenic plants with increased resistance to geminivirus infection  
PT comprise a nucleic acid construct containing a nucleic acid sequence  
PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
PT -  
XX  
XX  
PS Disclosure; Page 49; 73pp; English.  
XX  
XX The present sequence represents a mutant peptide, derived from a  
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
CC protein are used to produce transgenic plants. The mutation in AL1 is  
CC present in a ribosome binding region, and expression of mutant AL1  
CC protein imparts increased resistance to geminivirus infection in the  
CC plant. Mutant AL1 proteins are useful for producing plants having  
CC increased resistance or reduced sensitivity to a geminivirus such as  
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
CC virus, cotton leaf curl virus or beet curly top virus.  
XX  
SQ Sequence 70 AA;  
Query Match 92.0%; Score 335; DB 21; Length 70;  
Best Local Similarity 92.9%; Pred. No. 7.8e-35;  
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFPQHNLNSNL 60  
DB 1 TLVWGEAAVDGSRARGGCGTSDNDAALNASSKEEALQIIREKIPEKYLFPQHNLNSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70  
RESULT 9  
AAB18678  
ID AAB18678 standard; peptide; 70 AA.  
XX  
AC AAB18678;  
XX  
DT 22-JAN-2001 (first entry)  
XX  
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
XX  
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
KW ribosome binding region; resistance; geminivirus infection.  
XX  
OS Synthetic.  
OS Tomato golden mosaic virus.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 12 /note= "wild type residue replaced with Ala"  
FT Misc-difference 13 /note= "wild type residue replaced with Ala"  
FT Misc-difference 15 /note= "wild type residue replaced with Ala"  
FT  
XX  
PN WO2000054573-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 15-MAR-2000; 2000WO-US06759.  
XX  
PR 18-MAR-1999; 99US-0125004.  
PR 09-APR-1999; 99US-0289346.  
XX  
XX (UYNC-) UNIV NORTH CAROLINA STATE.  
XX

XX PI Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX DR WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Claim 53; Page 42-43; 73pp; English.  
 XX The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX Sequence 70 AA;

Query Match 91.8%; Score 334; DB 21; Length 70;  
 Best Local Similarity 91.4%; Pred. No. 1e-34;  
 Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TLVWGFQVDCRSARGCQTSNDLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 60  
 Db 1 TLVWGFQVDCRSARGCQTSNDLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 Db 61 DRIFDKTPEP 70

RESULT 10  
 AAB18689  
 ID AAB18689 standard; peptide; 70 AA.  
 AC AAB18689;  
 XX 22-JAN-2001 (first entry)  
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX Synthetic.  
 OS Tomato golden mosaic virus.  
 XX Key Location/Qualifiers  
 FH Misc-difference 22 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 23 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 23 /note= "wild type residue replaced with Ala"  
 XX WO200054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.  
 XX 09-APR-1999; 99US-0289346.  
 XX

PA (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Disclosure; Page 48-49; 73pp; English.  
 XX The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX Sequence 70 AA;

Query Match 91.5%; Score 333; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 1.4e-34;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TLVWGFQVDCRSARGCQTSNDLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 60  
 Db 1 TLVWGFQVDCRSARGCQTSNDLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 Db 61 DRIFDKTPEP 70

RESULT 11  
 AAB18680  
 ID AAB18680 standard; peptide; 70 AA.  
 AC AAB18680;  
 XX 22-JAN-2001 (first entry)  
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX Synthetic.  
 OS Tomato golden mosaic virus.  
 XX Key Location/Qualifiers  
 FH Misc-difference 42 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 43 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 44 /note= "wild type residue replaced with Ala"  
 XX WO200054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX



PN WO200054573-A1.  
 XX 21-SEP-2000.  
 PD 15-MAR-2000; 2000WO-US06759.  
 PF 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 PA Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 FT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Claim 52; Page 44; 73pp; English.  
 PS The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX SQ Sequence 70 AA;

Query Match 30.1%; Score 328; DB 21; Length 70;  
 Best Local Similarity 91.4%; Pred. No. 6e-34;  
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGCQTSNDLLLEALNASKEEALQIREKIPKYLFOFHNLSNL 60  
 DB 1 TLVWGEFQVDSRGSGCQTSNDAAEALNASKEEALQIREKIPAAALFOFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70

RESULT 14  
 AAB18683  
 ID AAB18683 standard; peptide; 70 AA.  
 AC AAB18683;  
 XX 22-JAN-2001 (first entry)  
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.  
 KW Synthetic.  
 OS Tomato golden mosaic virus.  
 XX Key Location/Qualifiers  
 PH Misc-difference 59  
 FT /note= "wild type residue replaced with Ala"  
 FT Misc-difference 61  
 FT /note= "wild type residue replaced with Ala"

FT Misc-difference 62  
 FT /note= "wild type residue replaced with Ala"  
 XX WO200054573-A1.  
 XX 21-SEP-2000.  
 PD 15-MAR-2000; 2000WO-US06759.  
 PF 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 PA Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 FT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Claim 53; Page 45; 73pp; English.

CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.

QY 1 TLVWGEFQVDSRGSGCQTSNDLLLEALNASKEEALQIREKIPKYLFOFHNLSNL 60  
 DB 1 TLVWGEFQVDSRGSGCQTSNDAAEALNASKEEALQIREKIPKYLFOFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 AALFDKTPPEP 70

Query Match 89.8%; Score 327; DB 21; Length 70;  
 Best Local Similarity 91.4%; Pred. No. 8.1e-34;  
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDSRGSGCQTSNDLLLEALNASKEEALQIREKIPKYLFOFHNLSNL 60  
 DB 1 TLVWGEFQVDSRGSGCQTSNDAAEALNASKEEALQIREKIPKYLFOFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 AALFDKTPPEP 70  
 RESULT 15  
 AAB18682  
 ID AAB18682 standard; peptide; 70 AA.  
 AC AAB18682;  
 XX 22-JAN-2001 (first entry)  
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.  
 KW Synthetic.  
 OS Tomato golden mosaic virus.  
 XX Key Location/Qualifiers  
 PH Misc-difference 52



FT /note= "wild type residue replaced with Ala"  
 FT Misc-difference 54  
 FT /note= "wild type residue replaced with Ala"  
 FT Misc-difference 55  
 FT /note= "wild type residue replaced with Ala"

XX  
 PN WO200054573-Al.

XX  
 PD 21-SEP-2000.

XX  
 PF 15-MAR-2000; 2000WO-US06759.

XX  
 PR 18-MAR-1999; 99US-0125004.

XX  
 PR 09-APR-1999; 99US-0289346.

XX  
 PA (UYN-) UNIV NORTH CAROLINA STATE.

XX  
 PI Hanley-Bowdoin L, Orozco BM, Kong L;

XX  
 DR WPI; 2000-618851/59.

XX  
 PT Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -

XX  
 PS Claim 53; Page 44-45; 73pp; English.

XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.

XX  
 SQ Sequence 70 AA;

Query Match 89.3%; Score 325; DB 21; Length 70;  
 Best Local Similarity 91.4%; Pred. No. 1.4e-33;  
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTNDLLLEALNASSKEEALQIIREKIPEKYLQFFHNLNSNL 60

Db 1 TLVWGEFQVDRSARGGCGTNDLLLEALNASSKEEALQIIREKIPEKYLQFFHNLNSNL 60

QY 61 DRIFDKTPEP 70

Db 61 DRIFDKTPEP 70

Search completed: December 23, 2003, 08:56:32  
 Job time : 33.6667 secs



Db 110 TIWGFQVQDGRSARGGQSANDSYAKALNADSIESTILKEQPKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70  
:|||||

Db 170 ERIFVKVPEP 179

RESULT 2  
US-08-838-151A-46  
; Sequence 46, Application US/08838151A  
; Patent No. 6291743  
; GENERAL INFORMATION:  
; APPLICANT: Stout, John T  
; APPLICANT: Luu, Hang T  
; APPLICANT: Maxwell, Douglas  
; APPLICANT: Ahlquist, Paul  
; APPLICANT: Hanson, Steve  
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
; TITLE OF INVENTION: Genes  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
; STREET: Two Prudential Plaza, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838,151A  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mueller, Lisa V  
; REGISTRATION NUMBER: 38,978  
; REFERENCE/DOCKET NUMBER: SVS3801P0260  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-616-5400  
; TELEFAX: 312-616-5400  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 353 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-838-151A-46

Query Match 61.3%; Score 223; DB 3; Length 353;  
Best Local Similarity 60.0%; Pred. No. 2.5e-21;  
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGFQVQDGRSARGGQTSNDLLEALNASSKEALQIREKIPEKYLFPQHNLNSNL 60  
:|||||

Db 110 TIWGFQVQDGRSARGGQSANDSYAKALNADSIESTILKEQPKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70  
:|||||

Db 170 ERIFVKVPEP 179

RESULT 3  
US-08-838-151A-49  
; Sequence 49, Application US/08838151A  
; Patent No. 6291743  
; GENERAL INFORMATION:  
; APPLICANT: Stout, John T  
; APPLICANT: Luu, Hang T  
; APPLICANT: Maxwell, Douglas  
; APPLICANT: Ahlquist, Paul

; APPLICANT: Hanson, Steve  
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
; TITLE OF INVENTION: Genes  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
; STREET: Two Prudential Plaza, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838,151A  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mueller, Lisa V  
; REGISTRATION NUMBER: 38,978  
; REFERENCE/DOCKET NUMBER: SVS3801P0260  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-616-5400  
; TELEFAX: 312-616-5400  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 353 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-838-151A-49

Query Match 61.3%; Score 223; DB 3; Length 353;  
Best Local Similarity 60.0%; Pred. No. 2.5e-21;  
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGFQVQDGRSARGGQTSNDLLEALNASSKEALQIREKIPEKYLFPQHNLNSNL 60  
:|||||

Db 110 TIWGFQVQDGRSARGGQSANDSYAKALNADSIESTILKEQPKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70  
:|||||

Db 170 ERIFVKVPEP 179

RESULT 4  
US-08-838-151A-52  
; Sequence 52, Application US/08838151A  
; Patent No. 6291743  
; GENERAL INFORMATION:  
; APPLICANT: Stout, John T  
; APPLICANT: Luu, Hang T  
; APPLICANT: Maxwell, Douglas  
; APPLICANT: Ahlquist, Paul  
; APPLICANT: Hanson, Steve  
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
; TITLE OF INVENTION: Genes  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
; STREET: Two Prudential Plaza, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-52

Query Match 61.3%; Score 223; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 2.5e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
Db 110 TIWGFQVDGRSARGGCGQSANDSYAKALNADSIESTILKEQPKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 5
US-08-838-151A-55
; Sequence 55, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; APPLICATION NUMBER: 800
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
; US-08-838-151A-55

Query Match 61.3%; Score 223; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 2.5e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
Db 110 TIWGFQVDGRSARGGCGQSANDSYAKALNADSIESTILKEQPKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 6
US-08-809-103B-2
; Sequence 2, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELETYPE: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-2

Query Match 60.7%; Score 221; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 4.8e-21;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LYWGFQVDGRSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNL 61
Db 111 LEWGFQVDGRSARGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLQHHNIRSNL 170

QY 62 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179
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Tue Dec 23 09:55:20 2003

us-09-289-346b-10.ra1

Db 171 KVFQVPPAP 179

## RESULT 7

US-08-809-103B-4  
; Sequence 4, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR95/01192  
; FILING DATE: 15-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PATCH, Andrew J  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-809-103B-4

Query Match 60.7%; Score 221; DB 3; Length 359;  
Best Local Similarity 56.5%; Pred. No. 4.8e-21;  
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVMGFEVDGRSARGGQTSNDLLEALNASSKEALQIIREKIPEKYLQFHNLSNLD 61  
Db 111 LEWGTFTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLFHFNINSNLD 170  
Qy 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

## RESULT 8

US-08-809-103B-6  
; Sequence 6, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR95/01192  
; FILING DATE: 15-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PATCH, Andrew J  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-809-103B-6

Query Match 60.7%; Score 221; DB 3; Length 359;  
Best Local Similarity 56.5%; Pred. No. 4.8e-21;  
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVMGFEVDGRSARGGQTSNDLLEALNASSKEALQIIREKIPEKYLQFHNLSNLD 61  
Db 111 LEWGTFTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLFHFNINSNLD 170  
Qy 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

## RESULT 9

US-08-809-103B-8  
; Sequence 8, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:

; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B

FILING DATE: 17-MAR-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94.11040  
FILING DATE: 15-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/FR95/01192  
FILING DATE: 15-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: PATCH, Andrew J.  
REGISTRATION NUMBER: 32,925  
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 521-2297  
TELEFAX: (703) 685-0573  
TELEX: 248425 EMBON  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-809-103B-8  
Query Match 60.7%; Score 221; DB 3; Length 359;  
Best Local Similarity 56.5%; Pred. No. 4.8e-21;  
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;  
QY 2 LVWGEFQVDRSARGGCGTSDNLLLEALNASSKBEALQIREKIPEKYLFOFHNLSNL 61  
Db 111 LEWGTQFQIDGRSARGGCGTANDAYAKAINAGSKQALDVKEIAPRDYVLHFNINSLD 170  
QY 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179  
RESULT 10  
US-08-838-151A-2  
Sequence 2, Application US/08838151A  
Patent No. 6291743  
GENERAL INFORMATION:  
APPLICANT: Stout, John T  
APPLICANT: Luu, Hang T  
APPLICANT: Maxwell, Douglas  
APPLICANT: Ahlquist, Paul  
APPLICANT: Hanson, Steve  
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
TITLE OF INVENTION: Genes  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
STREET: Two Prudential Plaza, Suite 4700  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,151A  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Mueller, Lisa V  
REGISTRATION NUMBER: 38,978  
REFERENCE/DOCKET NUMBER: SVS3801P0260  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5400  
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 361 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-838-151A-2  
Query Match 60.7%; Score 221; DB 3; Length 361;  
Best Local Similarity 57.1%; Pred. No. 4.8e-21;  
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;  
QY 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKBEALQIREKIPEKYLFOFHNLSNL 60  
Db 110 TIWGEFQIDGRSARGGCGTSANDSYAKALNASSVQSALAVLREEQPKDFVLQHNIRSNL 169  
QY 61 DRIEDKTPEP 70  
Db 170 ERIFAKAPEP 179  
RESULT 11  
US-08-838-151A-4  
Sequence 4, Application US/08838151A  
Patent No. 6291743  
GENERAL INFORMATION:  
APPLICANT: Stout, John T  
APPLICANT: Luu, Hang T  
APPLICANT: Maxwell, Douglas  
APPLICANT: Ahlquist, Paul  
APPLICANT: Hanson, Steve  
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
TITLE OF INVENTION: Genes  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
STREET: Two Prudential Plaza, Suite 4700  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,151A  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Mueller, Lisa V  
REGISTRATION NUMBER: 38,978  
REFERENCE/DOCKET NUMBER: SVS3801P0260  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5400  
TELEFAX: 312-616-5460  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 361 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-838-151A-4  
Query Match 60.7%; Score 221; DB 3; Length 361;  
Best Local Similarity 57.1%; Pred. No. 4.8e-21;  
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;  
QY 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKBEALQIREKIPEKYLFOFHNLSNL 60  
Db 110 TIWGEFQIDGRSARGGCGTSANDSYAKALNASSVQSALAVLREEQPKDFVLQHNIRSNL 169

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QY 61 DRIFDKTPEP 70
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Db 170 ERIFAKAPEP 179

RESULT 12
US-08-838-151A-6
; Sequence 6, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8

Query Match 60.7%; Score 221; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 4.8e-21;
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGCFQVDRSGRGCGQTSDNLLLEALNASKKEALQITREKIPKYLFOFHNLSNL 60
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Db 110 TIWGDGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREEQKDFVLQNHIRSNL 169

QY 61 DRIFDKTPEP 70
:|||||
Db 170 ERIFAKAPEP 179

RESULT 14
US-08-838-151A-24
; Sequence 24, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A

QY 61 DRIFDKTPEP 70
:|||||
Db 170 ERIFAKAPEP 179

RESULT 13
US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
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/ FILING DATE: 800  
/ CLASSIFICATION: 800  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Mueller, Lisa V  
/ REGISTRATION NUMBER: 38,978  
/ REFERENCE/DOCKET NUMBER: SVS3801P0260  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 312-616-5400  
/ TELEFAX: 312-616-5460  
/ INFORMATION FOR SEQ ID NO: 24:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 357 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
US-08-838-151A-24

Query Match 56.6%; Score 206; DB 3; Length 357;  
Best Local Similarity 63.9%; Pred. No. 4.6e-19;  
Matches 39; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 4 WGEFQVDGSRARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLNSNLDRI 63  
Db 111 FGVSDIGRSARGGQOSANDAYAEALNSGSKSEALNILEKAPKDYILOFHNLSSNLDRI 170

QY 64 F 64  
Db 171 F 171

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Job time : 12.6667 secs

RESULT 15  
US-08-838-151A-27  
/ Sequence 27, Application US/08838151A  
/ Patent No. 6291743  
/ GENERAL INFORMATION:  
/ APPLICANT: Stout, John T  
/ APPLICANT: Luu, Hang T  
/ APPLICANT: Maxwell, Douglas  
/ APPLICANT: Ahlquist, Paul  
/ APPLICANT: Hanson, Steve  
/ TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
/ NUMBER OF SEQUENCES: 63  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
/ STREET: Two Prudential Plaza, Suite 4700  
/ CITY: Chicago  
/ STATE: Illinois  
/ COUNTRY: U.S.A.  
/ ZIP: 60601  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/838,151A  
/ FILING DATE:  
/ CLASSIFICATION: 800  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Mueller, Lisa V  
/ REGISTRATION NUMBER: 38,978  
/ REFERENCE/DOCKET NUMBER: SVS3801P0260  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 312-616-5400  
/ TELEFAX: 312-616-5460  
/ INFORMATION FOR SEQ ID NO: 27:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 357 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
US-08-838-151A-27

Query Match 56.6%; Score 206; DB 3; Length 357;  
Best Local Similarity 63.9%; Pred. No. 4.6e-19;  
Matches 39; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 4 WGEFQVDGSRARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLNSNLDRI 63  
Db 111 FGVSDIGRSARGGQOSANDAYAEALNSGSKSEALNILEKAPKDYILOFHNLSSNLDRI 170

QY 64 F 64  
Db 171 F 171

Search completed: December 23, 2003, 08:59:36  
Job time : 12.6667 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds  
(without alignments)  
172.015 Million cell updates/sec

Title: US-09-289-346B-10  
Perfect score: 364  
Sequence: 1 TLVWGEFQVDRGARGCQT.....FQFHNLSNLDRIFDKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/FCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
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- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	364	100.0	70	10	US-09-289-346A-10
2	349	95.9	70	10	US-09-289-346A-1
3	349	95.9	356	10	US-09-289-346A-11
4	341	93.7	70	10	US-09-289-346A-9
5	338	92.9	70	10	US-09-289-346A-12
6	337	92.6	70	10	US-09-289-346A-16
7	335	92.0	70	10	US-09-289-346A-8
8	335	92.0	70	10	US-09-289-346A-14
9	334	91.8	70	10	US-09-289-346A-2
10	333	91.5	70	10	US-09-289-346A-13
11	331	90.9	70	10	US-09-289-346A-4
12	331	90.9	70	10	US-09-289-346A-15
13	328	90.1	70	10	US-09-289-346A-5
14	327	89.8	70	10	US-09-289-346A-7
15	325	89.3	70	10	US-09-289-346A-6

16	317	87.1	70	10	US-09-289-346A-3	Sequence 3, Appli
17	65	17.9	293	15	US-10-151-336-3	Sequence 3, Appli
18	65	17.9	335	15	US-10-151-336-6	Sequence 6, Appli
19	65	17.9	886	15	US-10-156-761-9112	Sequence 9112, Ap
20	64	17.6	712	11	US-09-893-519A-35	Sequence 35, Appl
21	64	17.6	722	12	US-10-032-585-7153	Sequence 7153, Ap
22	63	17.3	343	9	US-09-815-242-10474	Sequence 10474, A
23	62	17.0	21	10	US-09-984-056-17	Sequence 17, Appl
24	62	17.0	21	10	US-09-984-057-17	Sequence 17, Appl
25	62	17.0	21	12	US-10-105-232-17	Sequence 17, Appl
26	62	17.0	21	12	US-10-189-437-17	Sequence 17, Appl
27	62	17.0	272	9	US-09-804-969-19	Sequence 19, Appl
28	62	17.0	340	10	US-09-835-996A-19	Sequence 19, Appl
29	62	17.0	340	12	US-10-094-749-2976	Sequence 2976, Ap
30	62	17.0	567	10	US-09-835-996A-8	Sequence 8, Appli
31	62	17.0	759	15	US-10-258-860-6	Sequence 6, Appli
32	62	17.0	762	9	US-09-804-969-15	Sequence 15, Appl
33	62	17.0	762	10	US-09-908-664-2	Sequence 2, Appli
34	62	17.0	762	15	US-10-258-860-2	Sequence 4, Appli
35	62	17.0	785	15	US-10-258-860-4	Sequence 27, Appl
36	61.5	16.9	1279	12	US-09-882-227-388	Sequence 388, App
37	61	16.8	603	12	US-10-071-962-27	Sequence 27, Appli
38	61	16.8	836	11	US-09-972-708-9	Sequence 9, Appli
39	60.5	16.6	447	9	US-09-989-723-369	Sequence 369, App
40	60.5	16.6	447	9	US-09-989-723-369	Sequence 369, App
41	60.5	16.6	447	9	US-09-989-723-369	Sequence 369, App
42	60.5	16.6	447	9	US-09-989-723-369	Sequence 369, App
43	60.5	16.6	447	10	US-09-989-731-369	Sequence 369, App
44	60.5	16.6	447	10	US-09-989-732-369	Sequence 369, App
45	60.5	16.6	447	10	US-09-991-073-369	Sequence 369, App

ALIGNMENTS

RESULT 1

US-09-289-346A-10  
; Sequence 10, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (24)..(26)  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with leucine  
; OTHER INFORMATION: replacements (AAA136->LIL136).  
US-09-289-346A-10

Query Match	100.0%;	Score 364;	DB 10;	Length 70;
Best Local Similarity	100.0%;	Pred. No. 4.4e-39;		
Matches	70;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
Oy	1	TLVWGEFQVDRGARGCQTSNLLLEALNASSKEALQIIRKIKPKYLFQFHNLSNL	60	
Db	1	TLVWGEFQVDRGARGCQTSNLLLEALNASSKEALQIIRKIKPKYLFQFHNLSNL	60	
Oy	61	DRIFDKTPPEP	70	

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Db          61 DRIFDKTPEP 70
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RESULT 2
US-09-289-346A-1
; Sequence 1, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-1
Query Match          95.9%; Score 349; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 3.7e-37;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLQFQHNLSNL 60
Db 1 TLVWGEFQVDSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLQFQHNLSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
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RESULT 3
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11
Query Match          95.9%; Score 349; DB 10; Length 356;
Best Local Similarity 95.7%; Pred. No. 3.1e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLQFQHNLSNL 60
|||||
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```
Db          110 TLVWGEFQVDSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLQFQHNLSNL 169
QY 61 DRIFDKTPEP 70
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Db 170 DRIFDKTPEP 179
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RESULT 4
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9
Query Match          93.7%; Score 341; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 3.9e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLQFQHNLSNL 60
Db 1 TLVWGEFQVDSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLQFQHNLSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
|||||
RESULT 5
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12
Query Match          92.9%; Score 338; DB 10; Length 70;
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Best Local Similarity 92.9%; Pred. No. 9.4e-36;  
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60  
DB 1 TLVWGEFQVDRSARGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70

## RESULT 6

US-09-289-346A-16  
; Sequence 16, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
US-09-289-346A-16

Query Match 92.6%; Score 337; DB 10; Length 70;  
Best Local Similarity 92.9%; Pred. No. 1.3e-35;  
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60  
DB 1 TLVWGEFQVDRSARGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70

## RESULT 7

US-09-289-346A-8  
; Sequence 8, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (7)..(8)  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of

; OTHER INFORMATION: TMGV Rep Protein (aa 110-179) with alanine  
; OTHER INFORMATION: replacements (FQ118->A118).  
US-09-289-346A-8

Query Match 92.0%; Score 335; DB 10; Length 70;  
Best Local Similarity 92.9%; Pred. No. 2.3e-35;  
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60  
DB 1 TLVWGEAAVDGRSARGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70

## RESULT 8

US-09-289-346A-14  
; Sequence 14, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
US-09-289-346A-14

Query Match 92.0%; Score 335; DB 10; Length 70;  
Best Local Similarity 92.9%; Pred. No. 2.3e-35;  
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60  
DB 1 TLVWGEFQVDRSARGGCGTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70

## RESULT 9

US-09-289-346A-2  
; Sequence 2, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 70  
; TYPE: PRT

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; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
US-09-289-346A-2

Query Match          91.8%; Score 334; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 3.1e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-13

Query Match          91.5%; Score 333; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 4.1e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-4
; Sequence 4, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18

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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (42)..(44)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REK154->AAAA154).
US-09-289-346A-4

Query Match          90.9%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 7.4e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match          90.9%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 7.4e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS

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; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (EKY159->AAAA159).
US-09-289-346A-5

Query Match          90.1%; Score 328; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.8e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCOTSDNLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60
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Db 1 TLVWGEFQVDRSARGCGCOTSDNAAAEALNASSKEEALQIIREKIPAAALQFPHNLSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 14
US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (59)..(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDRI172->SALAA172).
US-09-289-346A-7

Query Match          89.8%; Score 327; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 2.4e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCOTSDNLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60
   |||||
Db 1 TLVWGEFQVDRSARGCGCOTSDNAAAEALNASSKEEALQIIREKIPKYLQFPHNLSAL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 AAFDKTPEP 70
   |||||
```

```
RESULT 15
US-09-289-346A-6
; Sequence 6, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (52)..(55)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (QFHN165->AFAA165).
US-09-289-346A-6

Query Match          89.3%; Score 325; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 4.4e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCOTSDNLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60
   |||||
Db 1 TLVWGEFQVDRSARGCGCOTSDNAAAEALNASSKEEALQIIREKIPKYLQFPHNLSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

Search completed: December 23, 2003, 09:43:32
Job time : 77 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 seconds  
(without alignments)  
673.181 Million cell updates/sec

Title: US-09-289-346B-10  
Perfect score: 364  
Sequence: 1 TLVWGFQVDSRGSGCQT.....FQHNLSNLDRIFDKTPPEP 70  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	349	95.9	352	1	QOCVLI	ALI protein - toma
2	249	68.4	361	1	QOCVPT	ALI protein - pota
3	242	66.5	358	2	S07594	hypothetical prote
4	235	64.6	362	1	JQ1887	ALI protein - toma
5	228	62.6	349	2	JQ2300	replicase - pepper
6	228	62.6	349	2	S31875	ALI protein - pepp
7	228	62.6	359	2	S39211	gene C1 protein -
8	221	60.7	359	2	S22593	hypothetical prote
9	220	60.4	355	1	QOCVW1	AVI protein - abut
10	218	59.9	351	2	JQ2327	ALI protein - indi
11	217	59.6	358	1	JQ1870	ALI protein - toma
12	217	59.6	385	2	S28360	ALI protein - beet
13	215	59.1	359	2	S39235	gene C1 protein -
14	208	57.1	360	2	S59885	replication-associ
15	206	56.6	357	1	QOCVC1	ALI protein - toma
16	138	37.9	131	2	S45059	ACI protein (clone
17	125	34.3	347	1	QOCVS1	ALI protein - squa
18	67	18.4	714	2	C95382	probable ferrichro
19	64	17.6	154	2	AD3475	protein-Npi-phosph
20	64	17.6	587	2	JC1419	Fc gamma (IgG) rec
21	63	17.4	1229	2	T48959	kinesin-like prote
22	63	17.3	343	2	A98295	ribosomal RNA smal
23	63	17.3	343	2	C86136	probable enzyme yj
24	63	17.3	343	2	S56595	rRNA (guanine-N2-)
25	62	17.0	295	2	D42452	C1 protein - tobac
26	62	17.0	329	2	D85956	hypothetical prote
27	62	17.0	329	2	A91111	hypothetical prote
28	62	17.0	416	2	A82892	hypothetical prote
29	61.5	16.9	333	2	B42476	hypothetical prote

30 61.5 16.9 333 2 AC0766  
31 61.5 16.9 481 2 A70091  
32 61.5 16.9 1279 2 E64709  
33 61 16.8 555 2 C45868  
34 61 16.8 771 2 B38252  
35 61 16.8 783 2 JH0329  
36 60.5 16.6 447 2 T12544  
37 60.5 16.6 447 2 T12544  
38 60.5 16.6 1792 2 T13939  
39 60 16.5 247 2 H86844  
40 60 16.5 470 2 T46814  
41 60 16.5 470 2 B95419  
42 60 16.5 799 2 T48889  
43 60 16.5 1117 2 T14891  
44 60 16.5 1265 2 T02131  
45 59.5 16.3 79 1 A58656

probable glycosylt  
probable phosphoe  
type IIS restricti  
glycerol-3-phospha  
granulocyte colony  
granulocyte colony  
granulocyte colony  
hypothetical prote  
myosin V - fruit f  
glutamine ABC tran  
gamma-aminobutyrat  
diaminobutyrate-py  
serine/threonine p  
telomerase (EC 2.7  
hypothetical prote  
adipokinetic hormo

## ALIGNMENTS

### RESULT 1

QOCVLI  
ALI protein - tomato golden mosaic virus  
C:Species: tomato golden mosaic virus  
A:Note: host Nicotiana sp. (tobacco)  
C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Apr-1994  
C:Accession: A04170  
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.  
EMBO J. 3, 2197-2205, 1984  
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat  
A:Reference number: A04163  
A:Accession: A04170  
A:Molecule type: DNA  
A:Residues: 1-352 <HAM>  
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 95.9%; Score 349; DB 1; Length 352;  
Best Local Similarity 95.7%; Pred. No. 1.7e-31;  
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 TLVWGFQVDSRGSGCQTSNDLLLEALNASKKEALQIIREKIPEKYLFOFHNLSNL 60  
Db 111 TLVWGFQVDSRGSGCQTSNDAAEALNASKKEALQIIREKIPEKYLFOFHNLSNL 170  
Qy 61 DRIFDKTPEP 70  
Db 171 DRIFDKTPEP 180

### RESULT 2

QOCVPT  
ALI protein - potato yellow mosaic virus (isolate Venezuela)  
C:Species: potato yellow mosaic virus  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jun-2000  
C:Accession: JU0364  
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.  
J. Gen. Virol. 72, 1515-1520, 1991  
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel  
A:Reference number: JU0362; UID:91311403; PMID:1856690  
A:Accession: JU0364  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-361 <COU>  
A:Cross-references: GB:D00940; NID:G222458; PIDN:BAA00782.1; PID:G222459  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus AL1 protein

```

Query Match      68.4%; Score 249; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 3e-20;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDLLLEALNASSKEALQIREKIPEKYLFOFHNLSNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TLEWGLFQIDGRSARGGCGTVDNAAEALNSGTKEAMKIIREKUPKFLFOFHNLSNL 169
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DRIFDKTPEP 69
   |||||:|||||
Db 170 DRIFMKAPE 178
   |||||:|||||

RESULT 3
S07594
Hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)
C:Species: cassava latent virus
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C:Accession: S07594
R:Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
Nucleic Acids Res. 18, 197-198, 1990
A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A:Reference number: S07590; MUID:90174930; PMID:2308831
A:Accession: S07594
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <MOR>
A:Cross-references: EMBL:X17095; NID:g59371; PIDN:CAA34953.1; PID:g59376
C:Genetics:
A:Map position: segment DNAL
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match      66.5%; Score 242; DB 2; Length 358;
Best Local Similarity 61.4%; Pred. No. 1.8e-19;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDLLLEALNASSKEALQIREKIPEKYLFOFHNLSNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 109 TVEWQFQIDGRSARGGCGQSANDYAKALNSGSKSEALNVLRELVPKDFVLOFHNLSNL 168
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DRIFDKTPEP 70
   |||||:|||||
Db 169 DRIFQEPAP 178
   |||||:|||||

RESULT 4
JQ1887
AL1 protein - tomato yellow leaf curl virus (strain Australia)
N:Alternate names: Cl protein
C:Species: tomato yellow leaf curl virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999
C:Accession: JQ1887
R:Dry, I.B.; Rigden, J.E.; Krake, L.R.; Mullineaux, P.M.; Rezaian, M.A.
J. Gen. Virol. 74, 147-151, 1993
A:Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.
A:Reference number: JQ1885; MUID:93139778; PMID:8423446
A:Accession: JQ1887
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <DRY>
A:Cross-references: GB:S53251
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match      64.6%; Score 235; DB 1; Length 362;
Best Local Similarity 54.1%; Pred. No. 1.1e-18;
Matches 46; Conservative 9; Mismatches 14; Indels 16; Gaps 1;

QY 1 TLVWGEFQVDRSARGGCGTSDLLLEALNASSKEALQIREKIPEKYLFOFHNLSNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 110 TLEWGEFQIDGRSARGGQSANDYAKALNTGSKSEALNVLRELAPKDFVLOFHNLSNL 169
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DRI-----FDKTPPE 69
   |||||:|||||

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```

Db 170 DRIFTPPLEVYVSPFLSSSDRVPPE 194

RESULT 5
JQ2300
replicase - pepper huasteco virus (component A)
N:Alternate names: ORF AL1 protein
C:Species: pepper huasteco virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Sep-1999
C:Accession: JQ2300
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Herrera-Estrella, L.; Rivera-Bustamante, R.
J. Gen. Virol. 74, 2225-2231, 1993
A:Title: Complete nucleotide of pepper huasteco virus: Analysis and comparison with bip
A:Reference number: JQ2299; MUID:94015007; PMID:8409944
A:Accession: JQ2300
A:Molecule type: DNA
A:Residues: 1-349 <TOR>
A:Cross-references: GB:X70418; NID:g61023; PIDN:CAA49856.1; PID:g61025
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match      62.6%; Score 228; DB 2; Length 349;
Best Local Similarity 60.0%; Pred. No. 6.7e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEALQIREKIPEKYLFOFHNLSNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 110 TVEWGEFQIDGRSARGGQSANDTYAKALNSAEEALQIIEQOPHFLOFHNIVSNA 169
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DRIFDKTPEP 70
   |||||:|||||
Db 170 NRIFQTPPEP 179
   |||||:|||||

RESULT 6
S31875
AL1 protein - pepper rizado amarillo virus
C:Species: pepper rizado amarillo virus
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 20-Sep-1999
C:Accession: S31875
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera-E
submitted to the EMBL Data Library, February 1993
A:Description: Complete nucleotide sequence of pepper huasteco virus: analysis and comp
A:Reference number: S31872
A:Accession: S31875
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <TOR>
A:Cross-references: EMBL:X70418; NID:g61023; PIDN:CAA49856.1; PID:g61025
A>Note: the source is designated as pepper huasteco virus
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match      62.6%; Score 228; DB 2; Length 349;
Best Local Similarity 60.0%; Pred. No. 6.7e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEALQIREKIPEKYLFOFHNLSNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 110 TVEWGEFQIDGRSARGGQSANDTYAKALNSAEEALQIIEQOPHFLOFHNIVSNA 169
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DRIFDKTPEP 70
   |||||:|||||
Db 170 NRIFQTPPEP 179
   |||||:|||||

RESULT 7
S39211
gene Cl protein - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C:Accession: S39211
R:Norris, E.; Hidalgo, E.; Accotto, G.; Moriones, E.
submitted to the EMBL Data Library, August 1993
A:Description: High similarity among the tomato yellow leaf curl virus isolates from th

```

A;Reference number: S39209

A;Accession: S39211

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-359 <NOR>

A;Cross-references: EMBL:Z25751; NID:q433655; PIDN:CAA81026.1; PID:q433658

C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 62.6%; Score 228; DB 2; Length 359;

Best Local Similarity 59.4%; Pred. No. 6.9e-18;

Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 2 LWGGEFQVDRSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNLD 61

DB 111 LEWTFQIDGRSARGGCGQTANDAYAKAINAGSKSEALDVIKELAPRDYILHFHNLSNLD 170

QY 62 RIFDKTPEP 70

DB 171 RVFQVPPAP 179

RESULT 8

S22593

Hypothetical protein C4 - tomato yellow leaf curl virus

C;Species: tomato yellow leaf curl virus

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Sep-1999

C;Accession: S22593

R;Kheyr-Pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.

Nucleic Acids Res. 19, 6763-6769, 1991

A;Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite

A;Reference number: S22588; MUID:92107660; PMID:1840676

A;Accession: S22593

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-359 <KHE>

A;Cross-references: EMBL:X61153; NID:G62211; PIDN:CAA43466.1; PID:G62217

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991

C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 60.7%; Score 221; DB 2; Length 359;

Best Local Similarity 56.5%; Pred. No. 4.2e-17;

Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LWGGEFQVDRSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNLD 61

DB 111 LEWTFQIDGRSARGGCGQTANDAYAKAINAGSKSQALDVIRELAPRDYILHFHNLSNLD 170

QY 62 RIFDKTPEP 70

DB 171 RVFQVPPAP 179

RESULT 9

QOCVW1

AV1 protein - abutilon mosaic virus (isolate West India)

C;Species: abutilon mosaic virus

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 08-Apr-1994

C;Accession: A36214

R;Frischmuth, T.; Zimmatt, G.; Jeske, H.

Virology 178, 461-468, 1990

A;Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as well

A;Reference number: A36214; MUID:91020984; PMID:2219703

A;Accession: A36214

A;Molecule type: DNA

A;Residues: 1-355 <PRI>

A;Cross-references: EMBL:X15993

C;Genetics:

A;Map position: segment A

C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match

Best Local Similarity 60.4%; Score 220; DB 1; Length 355;

Matches 41; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNLD 60

DB 110 TAEWGEFQIDGRSARGGCGQTANDSYAKALNAGDVQSALNILKEQPKDYVLQNHNRISNL 169

QY 61 DRIFDKTPEP 70

DB 170 ERIFAKAPEP 179

RESULT 10

JQ2327

AL1 protein - Indian cassava mosaic virus

N;Alternate names: replication-associated protein

C;Species: Indian cassava mosaic virus

C;Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 20-Sep-1999

C;Accession: JQ2327; S35883

R;Hong, Y.G.; Robinson, D.J.; Harrison, B.D.

J. Gen. Virol. 74, 2437-2443, 1993

A;Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-tr

A;Reference number: JQ2326; MUID:94065670; PMID:8245859

A;Accession: JQ2327

A;Molecule type: DNA

A;Residues: 1-351 <HON>

A;Cross-references: EMBL:Z24758; NID:G395351; PIDN:CAA80891.1; PID:G584046

C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.9%; Score 218; DB 2; Length 351;

Best Local Similarity 61.2%; Pred. No. 9e-17;

Matches 41; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 4 WGEFQVDRSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNLDRI 63

DB 113 WGTFTQIDGRSARGGCGQSANDAYAAALNSGSKALKILFELAPRDYILRDFHHISSNLDRI 172

QY 64 FDKTPEP 70

DB 173 FTKPPPP 179

RESULT 11

JQ1870

AL1 protein - tomato mottle virus (isolate Florida)

C;Species: tomato mottle virus

C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 07-May-1999

C;Accession: JQ1870

R;Abouzid, A.M.; Polston, J.E.; Hiebert, E.

J. Gen. Virol. 73, 3225-3229, 1992

A;Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated fr

A;Reference number: JQ1869; MUID:93107858; PMID:1469361

A;Accession: JQ1870

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-358 <ABO>

A;Cross-references: GB:I14460

C;Genetics:

A;Map position: segment A

C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match

Best Local Similarity 59.6%; Score 217; DB 1; Length 358;

Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEALQIIREKIPEKYLFOFHNLSNLD 60

DB 107 TIWGEFQIDGRSARGGCGQSANDSYAKALNAGSVQSALAVIREEQPKDYVLQNHNRISNL 166

QY 61 DRIFDKTPEP 70

DB 167 ERIFAKAPEP 176

RESULT 12





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds  
(without alignments)  
569.747 Million cell updates/sec

Title: US-09-289-346B-10

Perfect score: 364

Sequence: 1 TLVWGEFQVDRSARGGCQT.....QFHNLSNLDRIFDKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	349	95.9	352	1 VAL1_TGMV	P03567 tomato gold
2	249	68.4	361	1 VAL1_PYMV	P27258 potato yell
3	242	66.5	358	1 VAL1_CLVK	P14982 cassava lat
4	242	66.5	358	1 VAL1_CLVN	P14972 cassava lat
5	235	64.6	362	1 VAL1_TYLC	P36279 tomato yell
6	228	62.6	349	1 VAL1_PHVU	Q06923 pepper huas
7	228	62.6	359	1 VAL1_TYLC	P38609 tomato yell
8	221	60.7	353	1 VAL1_BGMV	P05175 bean golden
9	221	60.7	359	1 VAL1_TYLC	P27260 tomato yell
10	220	60.4	355	1 VAL1_ABMV	P21947 abutilon mo
11	217	59.6	358	1 VAL1_BCTV	P14991 beet curly
12	217	59.6	361	1 VAL1_TMOV	Q06657 tomato mott
13	206	56.6	357	1 VAL1_TYLC	P27259 tomato yell
14	125	34.3	347	1 VAL1_SLCV	P29048 squash leaf
15	63	17.3	342	1 RSMC_ECOLI	P39406 escherichia
16	62	17.0	150	1 DTD_STAEP	Q8CP01 staphylococ
17	62	17.0	295	1 VAL1_TYDV	P1617 tobacco yell
18	62	17.0	387	1 Y4PF_RHISN	P5615 rhizobium s
19	61	16.8	555	1 GLPD_EACSU	P18158 bacillus su
20	61	16.8	836	1 GCSR_HUMAN	Q99062 homo sapien
21	60.5	16.6	447	1 TBL2_HUMAN	Q9Y4P3 homo sapien
22	60	16.5	392	1 CL02_HUMAN	Q8NHQ8 homo sapien
23	60	16.5	470	1 RHA_RHIME	Q8Z3R2 r diaminobu
24	60	16.5	509	1 CA43_DROME	Q9VMS7 drosophila
25	60	16.5	799	1 AFSK_STRCO	P54741 streptomyce
26	60	16.5	807	1 AFSK_STRGR	P54742 streptomyce
27	60	16.5	1117	1 TERT_TERTH	O77448 tetrahymena
28	59.5	16.3	79	1 AKHD_DROME	P17975 drosophila
29	58.5	16.1	323	1 VAL1_PASVK	Q00338 panicum str
30	58.5	16.1	397	1 METL_RAT	P13444 rattus norv
31	58.5	16.1	1610	1 CCAD_MESAU	Q99244 mesocricetu
32	58.5	16.1	2161	1 CCAD_HUMAN	Q01668 homo sapien
33	58.5	16.1	2203	1 CCAD_RAT	P27732 rattus norv

## RESULT 1

VAL1\_TGMV 58 15.9 256 1 UT11\_YEAST P34247 saccharomyc  
AC P03567; 354 1 CARA\_METUA Q58425 methanococ  
DT 21-JUL-1986 (Rel. 01, Created) P07196 homo sapien  
DT 21-JUL-1986 (Rel. 01, Last sequence update) P35207 saccharomyc  
DT 01-JUN-1994 (Rel. 25, Last annotation update) P9W3C0 drosophila  
DE All protein. 38 57 15.7 237 1 UT11\_DROME Q9D92 rickettsia  
GN AC1. 39 57 15.7 784 1 LON\_RICPR Q21657 saccharomyc  
OS Tomato golden mosaic virus (TGMV). 40 57 15.7 970 1 DAB1\_YEAST P09130 campylobact  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus. 41 57 15.7 1517 1 RPOC\_CAMJTB Q8A194 euglena ana  
CX NCBI\_taxID=10631; 42 56.5 15.5 207 1 RPOA\_EUGAN Q8A194 euglena ana  
RN [1] 43 56.5 15.5 214 1 UT11\_ORYSA 08A121 oryza sativ  
RP SEQUENCE FROM N.A. 44 56.5 15.5 266 1 ETFB\_MYCLE O33095 mycobacteri  
RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.; 45 56.5 15.5 266 1 ETFB\_MYCTU O53276 mycobacteri  
RT "Complete nucleotide sequence of the infectious cloned DNA components  
of tomato golden mosaic virus: potential coding regions and regulatory  
sequences.";  
RL EMO J. 3:2197-2205 (1984).  
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.

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EMBL; K02029; -; NOT\_ANNOTATED\_CDS.  
PIR; A04170; Q0CVL1.  
InterPro; IPR001191; Gemini\_AL1.  
Pfam; PF00799; Gemini\_AL1; 1.  
PRINTS; PR00227; GEMCOATALL.  
ProDom; PD000736; Gemini\_AL1; 1.  
ATP-binding.  
NP\_BIND.  
SEQUENCE 352 AA; 40332 MW; C33C938B9644B4A4 CRC64;

Query Match 95.9%; Score 349; DB 1; Length 352;  
Best Local Similarity 95.7%; Pred. No. 1.5e-31;  
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSNDLLALNASSKEALQIIREKIPKYLQFHNLSNL 60  
Db 111 TLVWGEFQVDRSARGGCQTSNDAAALNASSKEALQIIREKIPKYLQFHNLSNL 170  
QY 61 DRIFDKTPPEP 70  
Db 171 DRIFDKTPPEP 180

RESULT 2  
VAL1\_PYMV STANDARD; PRT; 361 AA.  
AC P27258;

DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-AUG-1992 (Rel. 23, Last annotation update)  
DE AL1 protein.  
OS Potato yellow mosaic virus (isolate Venezuela).  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=10828;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91311403; PubMed=1856690;  
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;  
RT "the nucleotide sequence of the infectious cloned DNA components of  
potato yellow mosaic virus."  
RL J. Gen. Virol. 72:1515-1520(1991).  
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.  
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CC  
CC EMBL; D00940; BAA0782.1; -  
DR PIR; J00364; QOCVPT.  
DR InterPro; IPR001191; Gemini\_AL1.  
DR Pfam; PF00799; Gemini\_AL1; 1.  
DR PRINTS; PR00227; GEMCOATALL.  
DR ProDom; PD000736; Gemini\_AL1; 1.  
KW ATP-binding.  
FT NP\_BIND 222 229 ATP (POTENTIAL).  
SQ SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;  
  
Query Match 68.4%; Score 249; DB 1; Length 361;  
Best Local Similarity 66.7%; Pred. No. 2.2e-20;  
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;  
  
QY 1 TLVWGEFQVDRSGRGCGQTNDLLLEALNASSKEALQIIREKIPKYLQFHNLSNL 60  
DB 110 TIWGLFQIDGRSARGGQQTVDAAALNSGTREAAWKIKELPKFLQFHNLSNL 169  
QY 61 DRIFDKTPE 69  
DB 170 DRIFDKAPE 178  
  
RESULT 3  
VAL1\_CLVK  
ID VAL1 CLVK STANDARD; PRT; 358 AA.  
AC P14982;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE AL1 protein (40.4 kDa protein).  
GN AC1.  
OS Cassava latent virus (strain West Kenyan 844).  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=10818;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Stanley J., Gay M.R.;  
RT "Nucleotide sequence of cassava latent virus DNA.";  
RL Nature 301:260-262(1983).  
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.  
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CC

CC EMBL; J02057; -; NOT ANNOTATED CDS.  
DR InterPro; IPR001191; Gemini\_AL1.  
DR Pfam; PF00799; Gemini\_AL1; 1.  
DR PRINTS; PR00227; GEMCOATALL.  
DR ProDom; PD000736; Gemini\_AL1; 1.  
KW ATP-binding.  
FT NP\_BIND 220 227 ATP (POTENTIAL).  
SQ SEQUENCE 358 AA; 40346 MW; ED17E753EE92D69 CRC64;  
  
Query Match 66.5%; Score 242; DB 1; Length 358;  
Best Local Similarity 61.4%; Pred. No. 1.3e-19;  
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;  
  
QY 1 TLVWGEFQVDRSGRGCGQTNDLLLEALNASSKEALQIIREKIPKYLQFHNLSNL 60  
DB 109 TIWGLFQIDGRSARGGQQTVDAAALNSGTREAAWKIKELPKFLQFHNLSNL 168  
QY 61 DRIFDKTPE 70  
DB 169 DRIFQEPAP 178  
  
RESULT 4  
VAL1\_CLVN  
ID VAL1 CLVN STANDARD; PRT; 358 AA.  
AC P14972;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE AL1 protein (40.4 kDa protein).  
GN AC1.  
OS Cassava latent virus (strain Nigerian).  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=10819;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90174930; PubMed=2308831;  
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;  
RT "Nucleotide sequence of the infectious cloned DNA components of  
RT African cassava mosaic virus (Nigerian strain).";  
RL Nucleic Acids Res. 18:197-198(1990).  
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.  
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CC  
CC EMBL; X17095; CAA34953.1; -  
DR PIR; S07594; S07594.  
DR InterPro; IPR001191; Gemini\_AL1.  
DR Pfam; PF00799; Gemini\_AL1; 1.  
DR PRINTS; PR00227; GEMCOATALL.  
DR ProDom; PD000736; Gemini\_AL1; 1.  
KW ATP-binding.  
FT NP\_BIND 220 227 ATP (POTENTIAL).  
SQ SEQUENCE 358 AA; 40435 MW; 1DB16B0CB2D5E2C CRC64;  
  
Query Match 66.5%; Score 242; DB 1; Length 358;  
Best Local Similarity 61.4%; Pred. No. 1.3e-19;  
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;  
  
QY 1 TLVWGEFQVDRSGRGCGQTNDLLLEALNASSKEALQIIREKIPKYLQFHNLSNL 60  
DB 109 TIWGLFQIDGRSARGGQQTVDAAALNSGTREAAWKIKELPKFLQFHNLSNL 168  
QY 61 DRIFDKTPE 70  
DB 169 DRIFQEPAP 178

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RESULT 5
VAL1_TYLCU
ID VAL1_TYLCU STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AL1 protein (C1 protein).
GN Cl..
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36447;
RN [1]
RP SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;
RX MEDLINE=93139778; PubMed=8423446;
RA Dry I.B., Rigden J.E., Krake L.R., Mullineaux P.M., Rezaian M.A.;
RT "Nucleotide sequence and genome organization of tomato leaf curl
geminivirus."
RL J. Gen. Virol. 74:147-151 (1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR PIR: JQ1887; JQ1887.
DR InterPro: IPR001191; Gemini_A11.
DR Pfam: PF00799; Gemini_A11; I.
DR PRINTS: PR00227; GEMCOATALL1.
DR ProDom: PD000736; Gemini_A11; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;

Query Match 64.6%; Score 235; DB 1; Length 362;
Best Local Similarity 54.1%; Pred. No. 8.1e-19;
Matches 46; Conservative 9; Mismatches 14; Indels 16; Gaps 1;

Qy 1 TLVGEFQVDRSGRGCGQTNDLLLEALNASSKEALQIIREKIPKYLFOHNLNSL 60
Db 110 TLEWGEFQIDGRSARGGQQSANDAYACALNTGSKSEALNVRLAPKDYVLQFHNLSNL 169

Qy 61 DRI-----FDKTPPE 69
Db 170 DRIPTPELVVSPFLSSSFDVRPE 194

RESULT 6
VAL1_PHVU
ID VAL1_PHVU STANDARD; PRT; 349 AA.
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN Al1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tirnado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
comparison with bipartite geminiviruses."
RL J. Gen. Virol. 74:2225-2231 (1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC EMBL: X70418; CAA49856.1; -.
DR PIR: JQ2300; JQ2300.
DR PIR: S31875; S31875.
DR InterPro: IPR001191; Gemini_A11.
DR Pfam: PF00799; Gemini_A11; I.
DR PRINTS: PR00227; GEMCOATALL1.
DR ProDom: PD000736; Gemini_A11; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 39722 MW; DSF4E76CD56370F4 CRC64;

Query Match 62.6%; Score 228; DB 1; Length 349;
Best Local Similarity 60.0%; Pred. No. 4.7e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDRSGRGCGQTNDLLLEALNASSKEALQIIREKIPKYLFOHNLNSL 60
Db 110 TLEWGEFQIDGRSARGGQQSANDYAKALNSASAEALQIIRKQPQHFLOFHNIVSNA 169

Qy 61 DRIFDKTPPEP 70
Db 170 NRIFQTPEEP 179

RESULT 7
VAL1_TYLCU
ID VAL1_TYLCU STANDARD; PRT; 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 protein (C1 protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Norris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
from the west Mediterranean basin: the nucleotide sequence of an
infectious clone from Spain."
RL Arch. Virol. 135:165-170 (1994).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC EMBL: Z25751; CAA81026.1; -.
DR PIR: S39211; S39211.
DR InterPro: IPR001191; Gemini_A11.
DR Pfam: PF00799; Gemini_A11; I.
DR PRINTS: PR00227; GEMCOATALL1.
DR ProDom: PD000736; Gemini_A11; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3BC CRC64;

Query Match 62.6%; Score 228; DB 1; Length 359;
Best Local Similarity 59.4%; Pred. No. 4.8e-18;
Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVWGEFQVDRSGRGCGQTNDLLLEALNASSKEALQIIREKIPKYLFOHNLNSL 61
Db 111 LEWGTFFQIDGRSARGGQQTANDAYAKAINAGSKSEALDVIKELAPRDYILHFHNLSNL 170

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QY      62 RIFDKTPEP 70
DB      171 RVFQVPEAP 179

RESULT 8
VAL1_BGMV
ID VAL1_BGMV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE AL1 protein (40.2 kDa protein).
GN AC1
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Howarth A.J., Caton J., Bossert M., Goodman R.M.;
RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
  regulation in geminiviruses."
RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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DR EMBL; X61153; CAA43466.1; -
DR PIR; S22593; S22593.
DR PDB; 1L2M; 18-SEP-02.
DR PDB; 1L5I; 18-SEP-02.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding; 3D-structure.
FT NP BIND 220 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 60.7%; Score 221; DB 1; Length 353;
Best Local Similarity 60.0%; Pred. No. 2.8e-17;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY      1 TLVWGFQVDSRGSGCQTSNDLLLEALNASSKEEALQIREKIPEKYLFOFHNLSNL 60
DB      110 TLVWGFQVDSRGSGCQTSNDLLLEALNASSKEEALQIREKIPEKYLFOFHNLSNL 169

QY      61 DRIFDKTPEP 70
DB      170 ERIFKVPPEP 179

RESULT 9
VAL1_TYLCM
ID VAL1_TYLCM STANDARD; PRT; 359 AA.
AC P27250;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92107660; PubMed=1840676;
RA Kheyx-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
RA Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a

whitefly-transmitted monopartite geminivirus."
Nucleic Acids Res. 19:6763-6769(1991).
-!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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EMBL; X61153; CAA43466.1; -
PIR; S22593; S22593.
PDB; 1L2M; 18-SEP-02.
PDB; 1L5I; 18-SEP-02.
InterPro; IPR001191; Gemini_AL1.
Pfam; PF00799; Gemini_AL1; 1.
PRINTS; PR00227; GEMCOATALL.
ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding; 3D-structure.
FT NP BIND 220 229 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 40733 MW; 9717B4A07C93BEA7 CRC64;

Query Match 60.7%; Score 221; DB 1; Length 359;
Best Local Similarity 56.5%; Pred. No. 2.9e-17;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY      2 LVWGFQVDSRGSGCQTSNDLLLEALNASSKEEALQIREKIPEKYLFOFHNLSNL 61
DB      111 LVWGFQVDSRGSGCQTSNDLLLEALNASSKEEALQIREKIPEKYLFOFHNLSNL 170

QY      62 RIFDKTPEP 70
DB      171 KVQVPEAP 179

RESULT 10
VAL1_ABMVW
ID VAL1_ABMVW STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimmatt G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
  as well as eukaryotic features."
RL Virology 178:461-468(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
EMBL; X15983; -; NOT_ANNOTATED_CDS.
DR PIR; A36214; QOCVW1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.

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FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 355 AA; 40257 MW; 16A2CABA63251E95 CRC64;

Query Match 60.4%; Score 220; DB 1; Length 355;
Best Local Similarity 58.6%; Pred. No. 3.7e-17;
Matches 41; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 1 TLVNGEFQVGRSGGQTSNDLLLEALNASSKEALQIIRKIPKYLQFHNLSNL 60
Db 110 TAENGEFQIDGRSGGQTSNDLLLEALNASSKEALQIIRKIPKYLQFHNLSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 11
VAL1 BCTV STANDARD; PRT; 358 AA.
AC P14931;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein (40.8 kDa protein).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
CX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
beet curly top virus."
RL EMBO J. 5:1761-1767(1986).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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or send an email to license@isb-sib.ch).
CC
CC EMBL; L14460; AAC32414.1; -.
DR PIR; J01870; J01870.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALI.
DR ProDom; PD000736; Geminini_AL1; 1.
KW ATP-binding.
RN NP BIND 222 229 ATP (BY SIMILARITY).
RP SEQUENCE 351 AA; 40516 MW; 8138B65CEAC6950 CRC64;
SQ SEQUENCE 351 AA; 40516 MW; 8138B65CEAC6950 CRC64;

Query Match 59.6%; Score 217; DB 1; Length 361;
Best Local Similarity 55.7%; Pred. No. 8.2e-17;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVNGEFQVGRSGGQTSNDLLLEALNASSKEALQIIRKIPKYLQFHNLSNL 60
Db 110 TIENGDFQIDGRSGGQTSNDLLLEALNASSKEALQIIRKIPKYLQFHNLSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 12
VAL1 TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (C1 protein).
GN Cl.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
CX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92024070; PubMed=1926771;
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
with a single genomic component."
RL Virology 185:151-161(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC

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DR EMBL; X15856; CAA33688.1; -.
DR PIR; D40779; QQCVC1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding. 219 226 ATP (POTENTIAL).
FT NP_BIND 357 AA; 40678 MW; 939AB68E1AB3E2A7 CRC64;
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3E2A7 CRC64;

Query Match 56.6%; Score 206; DB 1; Length 357;
Best Local Similarity 63.9%; Pred. No. 1.4e-15;
Matches 39; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 4 WGEFQVDSRGSGCQTNDLLLEALNASSKEEALQIIRKIPKYLFOFHNLNSLDRI 63
DB 111 FGVSQIDGSRSGGQGSANDAYEALNSGSKSEALNILKRAKPYDILQFHLNSLDRI 170

QY 64 F 64
DB 171 F 171

RESULT 14
VAL1_SLCV STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE AL1 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G.; Lazdins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic components of a bipartite squash leaf curl geminivirus with a broad host range phenotype."
RT Virology 180:58-69(1991).
RL [1]
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
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CC
DR EMBL; M38183; AAC32410.1; ALT_INIT.
DR PIR; C36785; QQCVC1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding. 218 225 ATP (POTENTIAL).
FT NP_BIND 347 AA; 39110 MW; AFDABDE122110E CRC64;
SQ SEQUENCE 347 AA; 39110 MW; AFDABDE122110E CRC64;

Query Match 34.3%; Score 125; DB 1; Length 347;
Best Local Similarity 37.9%; Pred. No. 1.4e-06;
Matches 25; Conservative 15; Mismatches 22; Indels 4; Gaps 1;

QY 5 GEFQVDSRGSGCQTNDLLLEALNASSKEEALQIIRKIPKYLFOFHNLNSLDRI 64
DB 116 GQYKVSQ----GSKSNKDDVYHNAVAGSAGEALDIKAGDKPTIVYHNLNVERLF 171

QY 65 DKTPEP 70
DB 172 QKPEP 177

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RESULT 15
RSMC_ECOLI STANDARD; PRT; 342 AA.
AC P39406;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosomal RNA small subunit methyltransferase C (EC 2.1.1.52) (rRNA (guanine-N(2)-methyltransferase) (16S rRNA m2G1207 methyltransferase)).
DE RSMC OR B4371.
GN RSMC coli.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D.; Plunkett G. III; Sofia H.J.; Daniels D.L.;
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes."
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [2]
RP SEQUENCE OF 1-19, AND CHARACTERIZATION.
RX MEDLINE=99091632; PubMed=9873033;
RA Tscherne J.S.; Nurse K.; Popienick P.; Ofengand J.; 16S RNA m2G1207
RT "Purification, cloning, and characterization of the 16S RNA m2G1207 methyltransferase from Escherichia coli."
RL J. Biol. Chem. 274:924-929(1999).
CC -1- FUNCTION: SPECIFICALLY METHYLATES THE GUANOSINE IN POSITION 1207 OF 16S RNA IN THE 30S PARTICLE.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + rRNA = S-adenosyl-L-homocysteine + rRNA containing N(2)-methylguanine.
CC -1- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY. RSMC SUBFAMILY.
CC
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CC
DR EMBL; U14003; AAA97267.1; -.
DR EMBL; AE000507; AAC77324.1; -.
DR PIR; S56595; S56595.
DR EcoGene; EG12596; rsmC.
DR InterPro; IPR002296; N12N6_mtfase.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF05175; MTS_2.
DR PRINTS; PR00507; N12N6MTFRASE.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
KW rRNA processing; transferase; Methyltransferase; Magnesium;
FT INIT MET 0
SQ SEQUENCE 342 AA; 37493 MW; C7A318155700302D CRC64;

Query Match 17.3%; Score 63; DB 1; Length 342;
Best Local Similarity 31.1%; Pred. No. 11;
Matches 14; Conservative 7; Mismatches 16; Indels 8; Gaps 1;

QY 4 WGEFQVDSRGSGCQTNDLLLEALNASSKEEALQI 40
DB 158 WGEYSVDGLTVKTLPGVFSRDGLDVGSQLLTSTLTHTKGVLDV 202

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Search completed: December 23, 2003, 08:57:41  
Job time : 6.77778 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 25.3333 Seconds  
(without alignments)  
713.040 Million cell updates/sec

Title: US-09-289-346B-10

Perfect score: 364

Sequence: 1 TLVWGFQVDRSGARGCQT.....FQHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300	82.4	351	Q91R10	Q91R10 tomato seve
2	298	81.9	352	Q9E000	Q9E000 tomato rugo
3	290	79.7	232	Q8QPV3	Q8QPV3 tomato chlo
4	281	77.2	226	Q9WHF6	Q9WHF6 tomato mild
5	281	77.2	226	Q09727	Q09727 leonurus mo
6	281	77.2	361	Q67574	Q67574 bean golden
7	279	76.6	225	Q9QDB1	Q9QDB1 cowpea gold
8	277	76.1	314	Q9ELT8	Q9ELT8 sweet potat
9	277	76.1	364	Q9Q555	Q9Q555 sweet potat
10	274	75.3	185	Q98693	Q98693 sida golden
11	272	74.7	235	Q8QPU4	Q8QPU4 tomato infe
12	269	73.9	208	Q8JLY3	Q8JLY3 potato yell
13	269	73.9	289	Q8JLY5	Q8JLY5 potato yell
14	266	73.1	149	Q88975	Q88975 macroptiliu
15	266	73.1	233	Q9YLA4	Q9YLA4 macroptiliu
16	265	72.8	361	Q8JMJ4	Q8JMJ4 potato yell

17	263	72.3	360	12	Q8QMH4	Q8QMH4 sida mottle
18	261	71.7	190	12	Q9Z089	Q9Z089 tobacco lea
19	261	71.7	190	12	Q9Z084	Q9Z084 tobacco lea
20	261	71.7	361	12	Q9QVH0	Q9QVH0 ageratum en
21	260	71.4	190	12	Q9W827	Q9W827 tobacco lea
22	260	71.4	208	12	Q9Z0C4	Q9Z0C4 tobacco lea
23	260	71.4	234	12	Q91R10	Q91R10 geminivirid
24	260	71.4	359	12	Q91M88	Q91M88 tobacco lea
25	260	71.4	359	12	Q8JVE8	Q8JVE8 tomato curl
26	258	70.9	208	12	Q9Z0C0	Q9Z0C0 tobacco lea
27	258	70.9	208	12	Q9Z0B8	Q9Z0B8 tobacco lea
28	258	70.9	223	12	Q8QPU7	Q8QPU7 tomato seve
29	256	70.3	208	12	Q9Z0B6	Q9Z0B6 tobacco lea
30	255	70.1	203	12	Q9Z083	Q9Z083 tobacco lea
31	251	69.0	363	12	Q73577	Q73577 cotton leaf
32	250	68.7	363	12	Q72719	Q72719 cotton leaf
33	250	68.7	363	12	Q72705	Q72705 cotton leaf
34	249	68.4	349	12	Q88888	Q88888 tomato pseu
35	248	68.1	208	12	Q9Z0A0	Q9Z0A0 tobacco lea
36	248	68.1	348	12	Q911W5	Q911W5 macroptiliu
37	247	67.9	190	12	Q9Z086	Q9Z086 tobacco lea
38	247	67.9	208	12	Q9Z0C6	Q9Z0C6 tobacco lea
39	247	67.9	359	12	Q9YZV4	Q9YZV4 tomato yell
40	247	67.9	359	12	Q9YUX7	Q9YUX7 tomato yell
41	247	67.9	359	12	Q9YL27	Q9YL27 tomato yell
42	247	67.9	359	12	Q9YZV2	Q9YZV2 tomato yell
43	246	67.6	359	12	Q8JNG3	Q8JNG3 tomato leaf
44	246	67.6	359	12	Q88942	Q88942 tomato yell
45	246	67.6	359	12	Q91B86	Q91B86 ageratum ye

#### ALIGNMENTS

RESULT 1

Q91R10 PRELIMINARY; PRT; 351 AA.

AC Q91R10, 2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)

DE Rep protein.

GN ACL.

OS Tomato severe rugose virus.

OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

OX NCHI\_TaxID=158463;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Minas Gerais;

RA Rezende W.L., Goulart L.R., Parreira K.S., Figueiredo J.E.F.;

RT "The full-length DNA-A nucleotide sequence of a novel tomato-infecting begomovirus, Tomato severe rugose virus, in Brazil.";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY029750; AAK50357.1;

DR InterPro; IPR001191; Gemini\_AL1.

DR Pfam; PF00799; Gemini\_AL1; 1.

DR PRINTS; PR00227; GEMCOATALL.

DR ProDom; PD000736; Gemini\_AL1; 1.

SQ SEQUENCE 351 AA; 40122 MW; 87F937A4F873B6CF CRC64;

Query Match 82.4%; Score 300; DB 12; Length 351;  
Best Local Similarity 78.6%; Pred. NO. 3.5e-26;  
Matches 55; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGARGCQTNDLLLEALNASKKEALQIIREKIPEKYLQFHNLSNL 60

Db 111 TIWGFQIDGRSGCQTANDAAAEALNAPSQVALQIIREKLEKLEKLFQFHNLSNL 170

QY 61 DRIFDKTPEP 70

Db 171 DRIFARAPEP 180



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SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E765083PC5 CRC64;
Query Match 77.2%; Score 281; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 3.2e-24;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGFQVQDGRSARGCGCOTSDNLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
Db 111 TVWGFQVQDGRSARGCGCOTSDNLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 170

QY 61 DRIFDKTPPEP 70
Db 171 DRIFAKAPEP 180

RESULT 6
ID Q67574 PRELIMINARY; PRT; 361 AA.
AC Q67574;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Putative replicative protein.
GN Ali.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN 1
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration."
RL Phytopathology 81:980-985(1991).
RN 12
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RT "Differentiation of bean-infecting geminiviruses by nucleic acid
RT hybridization probes and aspects of bean golden mosaic in Brazil."
RL Plant Dis. 75:336-342(1991).
RN 3
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus."
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M88686; AAA46312.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 77.2%; Score 281; DB 12; Length 361;
Best Local Similarity 77.6%; Pred. No. 5.6e-24;
Matches 52; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 WGFQVQDGRSARGCGCOTSDNLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 63
Db 113 WGFQVQDGRSARGCGCOTSDNLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 172

QY 64 FDKTPPEP 70
Db 173 FTRAFDP 179

RESULT 7
ID Q9QDB1 PRELIMINARY; PRT; 225 AA.
AC Q9QDB1;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Putative replicative protein.
GN Ali.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN 1
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration."
RL Phytopathology 81:980-985(1991).
RN 12
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RT "Differentiation of bean-infecting geminiviruses by nucleic acid
RT hybridization probes and aspects of bean golden mosaic in Brazil."
RL Plant Dis. 75:336-342(1991).
RN 3
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus."
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M88686; AAA46312.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 77.2%; Score 281; DB 12; Length 361;
Best Local Similarity 77.6%; Pred. No. 5.6e-24;
Matches 52; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 WGFQVQDGRSARGCGCOTSDNLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 63
Db 113 WGFQVQDGRSARGCGCOTSDNLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 172

QY 64 FDKTPPEP 70
Db 173 FTRAFDP 179

RESULT 8
ID Q9ELT8 PRELIMINARY; PRT; 314 AA.
AC Q9ELT8;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Replication association protein.
GN Acl.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN 1
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States."
RL Plant Dis. 82:1253-1257(1998).
RN 12
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288227; AAG01006.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 76.1%; Score 277; DB 12; Length 314;
Best Local Similarity 79.4%; Pred. No. 1.4e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGFQVQDGRSARGCGCOTSDNLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
Db 110 TLVWGFQVQDGRSARGCGCOTSDNLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 169

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DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Cowpea golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN 1
RP SEQUENCE FROM N.A.
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RT Brazil."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF188708; AAF06318.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 225
SQ SEQUENCE 225 AA; 25766 MW; 1089CB6BD8D15B5D CRC64;

Query Match 76.8%; Score 279; DB 12; Length 225;
Best Local Similarity 77.6%; Pred. No. 5.4e-24;
Matches 52; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 4 WGFQVQDGRSARGCGCOTSDNLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 63
Db 113 WGFQVQDGRSARGCGCOTSDNLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 172

QY 64 FDKTPPEP 70
Db 173 FKKEPPEP 179

RESULT 8
ID Q9ELT8 PRELIMINARY; PRT; 314 AA.
AC Q9ELT8;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Replication association protein.
GN Acl.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN 1
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States."
RL Plant Dis. 82:1253-1257(1998).
RN 12
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288227; AAG01006.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 76.1%; Score 277; DB 12; Length 314;
Best Local Similarity 79.4%; Pred. No. 1.4e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGFQVQDGRSARGCGCOTSDNLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
Db 110 TLVWGFQVQDGRSARGCGCOTSDNLLLEALNASSKEALQIIREKIPKYLFOFHNLSNL 169

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QY      61 DRIFDKTP 68
Db      170 DRIFSPPP 177

RESULT 9
Q9Q555 PRELIMINARY; PRT; 364 AA.
AC Q9Q555;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RT virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0(1999).
DR EMBL; AF104036; A047173.1; -.
DR InterPro; IPR001191; Gemin_A11.
DR Pfam; PF00799; Gemin_A11; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemin_A11; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 76.1%; Score 277; DB 12; Length 364;
Best Local Similarity 79.4%; Pred. No. 1.6e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY      1 TLVWGFEQVQDGRSARGGCGTQNDLLLEALNASSKEALQIIREKIPEKYLQFQHNLSNL 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TITWGFQVQDGRSARGGCGTQNDAAAEALNAGSKEALQIIREKLPERKLFQYHNSL 169
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      61 DRIFDKTP 68
Db      170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica;
RC Roye M.E., McLaughlin W.A., Nakha N.K., Maxwell D.P.;
RT "Genetic Diversity among geminiviruses associated with the weed
RT species Sida spp, Macroptilium lathyroides, and Wissadula amplissima
RT from Jamaica."
RL Plant Dis. 81:1251-1258(1997).
DR EMBL; U67926; AAB97865.1; -.
DR InterPro; IPR001191; Gemin_A11.
DR Pfam; PF00799; Gemin_A11; 1.
DR PRINTS; PR00227; GEMCOATL1.

QY      1 TLVWGFEQVQDGRSARGGCGTQNDLLLEALNASSKEALQIIREKIPEKYLQFQHNLSNL 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TITWGFQVQDGRSARGGCGTQNDAAAEALNAGSKEALQIIREKLPERKLFQYHNSL 169
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      61 DRIFDKTP 68
Db      170 DRIFSPPP 177

RESULT 11
Q8QPU4 PRELIMINARY; PRT; 235 AA.
AC Q8QPU4;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RA Ribeiro S.G., Ambrozovicius L.P., de Avila A.C., Calegario R.F.,
RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini P.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049208; AAL82833.1; -.
DR InterPro; IPR001191; Gemin_A11.
DR Pfam; PF00799; Gemin_A11; 1.
DR ProDom; PD000736; Gemin_A11; 1.
DR NON TER 235 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BE0DDC810 CRC64;

Query Match 74.7%; Score 272; DB 12; Length 235;
Best Local Similarity 74.6%; Pred. No. 3.6e-23;
Matches 50; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY      4 WGEFQVQDGRSARGGCGTQNDLLLEALNASSKEALQIIREKIPEKYLQFQHNLSNL 63
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      113 WGFQVQDGRSARGGCGTQNDAAAEALNASSKEALQIIREKLPERKLFQYHNSL 172
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      64 FDKTPEP 70
Db      173 FTKAPDP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

```



Search completed: December 23, 2003, 09:03:37  
Job time : 25.3333 sec

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds  
(without alignments)  
340.128 Million cell updates/sec

Title: US-09-289-346B-2

Perfect score: 162

Sequence: 1 TLVWGFQVDDAAAGGCQT.....FQFHNLSNLDRIFDKTPET 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1980.DAT.\*
- 2: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1981.DAT.\*
- 3: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1982.DAT.\*
- 4: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1983.DAT.\*
- 5: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1984.DAT.\*
- 6: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1985.DAT.\*
- 7: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1986.DAT.\*
- 8: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1987.DAT.\*
- 9: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1988.DAT.\*
- 10: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1989.DAT.\*
- 11: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1990.DAT.\*
- 12: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1991.DAT.\*
- 13: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1992.DAT.\*
- 14: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1993.DAT.\*
- 15: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1994.DAT.\*
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- 19: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1998.DAT.\*
- 20: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA1999.DAT.\*
- 21: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA2000.DAT.\*
- 22: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA2001.DAT.\*
- 23: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA2002.DAT.\*
- 24: /SIDSL1/gcgdata/geneseq/genesecp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	362	100.0	70	21	AA18678
2	349	96.4	70	21	AA18677
3	349	96.4	356	21	AA18687
4	341	94.2	70	21	AA18685
5	338	93.4	70	21	AA18688
6	337	93.1	70	21	AA18692
7	335	92.5	70	21	AA18684
8	335	92.5	70	21	AA18690
9	334	92.3	70	21	AA18686

10	333	92.0	70	21	AA18689	Mutant peptide der
11	331	91.4	70	21	AA18680	Mutant peptide der
12	331	91.4	70	21	AA18691	Mutant peptide der
13	328	90.6	70	21	AA18681	Mutant peptide der
14	327	90.3	70	21	AA18683	Mutant peptide der
15	325	89.8	70	21	AA18682	Mutant peptide der
16	317	87.6	70	21	AA18679	Mutant peptide der
17	233.5	61.7	50	23	AAO22043	Retinoblastoma-bin
18	215	59.4	353	18	AAW34338	Bean golden mosaic
19	215	59.4	353	18	AAW34332	Bean golden mosaic
20	215	59.4	353	18	AAW34333	Bean golden mosaic
21	215	59.4	353	18	AAW34334	Bean golden mosaic
22	215	59.4	353	18	AAW34335	Bean golden mosaic
23	215	59.4	359	17	AAW34336	Sardinian tomato y
24	215	59.4	359	17	AAW34337	Sardinian tomato y
25	215	59.4	359	17	AAW34338	Sardinian tomato y
26	213	58.8	361	18	AAW34339	ORF 4 gene product
27	213	58.8	361	18	AAW34340	Tomato mottle viru
28	213	58.8	361	18	AAW34341	Tomato mottle viru
29	213	58.8	361	18	AAW34342	Tomato mottle viru
30	213	58.8	361	18	AAW34343	Tomato mottle viru
31	206.5	57.0	361	8	AAW34344	Product of ORF 4 f
32	201	55.5	362	19	AAW34345	Tobacco leaf curl
33	200	55.2	357	18	AAW34346	Tomato yellow leaf
34	200	55.2	357	18	AAW34347	Tomato yellow leaf
35	200	55.2	357	18	AAW34348	Tomato yellow leaf
36	192	53.0	357	18	AAW34349	Tomato yellow leaf
37	89	24.6	142	24	ABP58120	Tomato yellow leaf
38	81.5	22.5	945	22	ABP58121	Drosophila melanog
39	69.5	19.2	512	19	AAW68473	HIV-1 strain YBF30
40	68.5	18.9	1693	21	AAW68474	Human laminin 5 po
41	68.5	18.9	1693	21	AAW68475	Human laminin 5 po
42	68.5	18.9	1713	16	AAW70148	Deduced sequence o
43	68.5	18.9	1713	21	AAW70149	Deduced sequence o
44	68.5	18.9	1724	21	AAW70150	Human laminin 5 po
45	66.5	18.4	665	22	ABW70991	Drosophila melanog

ALIGNMENTS

RESULT 1

A.318678

ID AA18678 standard; peptide; 70 AA.

XX AA18678;

AC AA18678;

XX

DT 22-JAN-2001 (first entry)

XX

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

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DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

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DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

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DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

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DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX

XX PA (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX PI Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX DR WPI; 2000-618851/59.  
 XX PT Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX  
 XX PS Claim 53; Page 42-43; 73pp; English.  
 XX CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX SQ Sequence 70 AA;  
 Query Match 100.0%; Score 362; DB 21; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-37;  
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDGAAAGCGCOTSDNDAAEALNASSKEALQIREKIPEKYLFOFHNLSNL 60  
 DB 1 TLVWGEFQVDGAAAGCGCOTSDNDAAEALNASSKEALQIREKIPEKYLFOFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 2  
 AAB18677  
 ID AAB18677 standard; peptide; 70 AA.  
 AC AAB18677;  
 XX 22-JAN-2001 (first entry)  
 DE Peptide fragment from Rep protein of TGMV (amino acids 110-179).  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX Tomato golden mosaic virus.  
 OS  
 XX WO200054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.  
 XX 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX DR

XX PT Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX  
 XX PS Disclosure; Page 18; 73pp; English.  
 XX CC The present sequence is derived from a geminivirus replication (Rep)  
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,  
 CC catalyzes cleavage and ligation of single-stranded DNA, and interacts  
 CC with other viral and host proteins. Mutants of the AL1 protein are used  
 CC to produce transgenic plants. The mutation in AL1 is present in a  
 CC ribosome binding region, and expression of mutant AL1 protein imparts  
 CC increased resistance to geminivirus infection in the plant. Mutant AL1  
 CC proteins are useful for producing plants having increased resistance or  
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,  
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl  
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato  
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,  
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or  
 CC beet curly top virus.  
 XX SQ Sequence 70 AA;  
 Query Match 96.4%; Score 349; DB 21; Length 70;  
 Best Local Similarity 95.7%; Pred. No. 2.3e-35;  
 Matches 67; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDGAAAGCGCOTSDNDAAEALNASSKEALQIREKIPEKYLFOFHNLSNL 60  
 DB 1 TLVWGEFQVDGSRARGCGCOTSDNDAAEALNASSKEALQIREKIPEKYLFOFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 3  
 AAB18687  
 ID AAB18687 standard; peptide; 356 AA.  
 AC AAB18687;  
 XX 22-JAN-2001 (first entry)  
 DE Amino acid sequence of a geminivirus replication protein of TGMV.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX Tomato golden mosaic virus.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 354  
 FT /note= "unspecified amino acid"  
 XX WO200054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.  
 XX 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection





[illegible]

SQ Sequence 70 AA; Query Match 93.1%; Score 337; DB 21; Length 70; Best Local Similarity 92.9%; Pred. NO. 6.8e-34; Matches 65; Conservative 1; Mismatches 4; Indels 0; Caps 0;

	matches	65; conserved	1; mismatches	4; indels	0; gaps
Qy	1	TLVGFQVDGAAAGGCGTSDNAAAEALNASSKEEALQIREKIPEKYLQFQHNLSNL	60		
Db	1	TLVGFQVDGSRGGCGTSDNAAAEALNASSKEEALQIREKIPEKYLQFQHNLSNL	60		

DS	1	ILVWGEFQVLDGRK
Qy	61	DRIFDKTPEP 70
Db	61	DRIFDATPAP 70

RESULT 7  
AAB18684  
ID AAB18684 standard; peptide: 70 AA.

AC AAB18684;  
XX  
DT 22-JAN-2001 (first entry)

DT	22-JAN-2001 (first entry)
DE	Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX	
KW	Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW	ribosome binding region; resistance; geminivirus infection.

OS  
XX  
NR  
Synthetic  
Ribosome

OS Tomato golden mosaic virus.

XX	Key	Location/Qualifiers
FH		

PT Misc-difference 7

FT	/note= "wild type residue replaced with Ala"
1	
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FT	Misc-difference 8	FT
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100	100	100

## XXIX

XX PN WO200054573-A1.

XX  
XX  
-573333-70M W3

PD 21-SEP-2000.

XX  
15-MAR-2000. 2000WC--180657E9

PF 15-MAR-2000; 2000WO-US06759.  
XX

PR 18-MAR-1999; 99US-0125004.

PR 09-APR-1999; 99US-0289346..

XX  
DA (ITUNC - ) UNITV NORTH CAROLINA STATE  
XX

PA (UYNCL) UNIV NORTH CAROLINA STATE.  
XX

PI Hanley-Bowdoin L, Orozco BM, Kong L;

[illegible]

DR WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX  
 PS Claim 52; Page 45; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;  
 Query Match 92.5%; Score 335; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 1.2e-33;  
 Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TLWGEFQVGGAAAGCGCOTSDNDAAEALNASSKEEALQIIRKIPKYLFOFHNLSNL 60  
 DB 1 TLWGEAAVGGRSARGCGCOTSDNDAAEALNASSKEEALQIIRKIPKYLFOFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 8  
 AAB18690  
 ID AAB18690 standard; peptide; 70 AA.  
 AC AAB18690;  
 XX  
 XX 22-JAN-2001 (first entry)  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 27 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 30 /note= "wild type residue replaced with Ala"  
 FT  
 XX  
 XX WO200054573-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 XX 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX

DR WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX  
 PS Disclosure; Page 49; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;  
 Query Match 92.5%; Score 335; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 1.2e-33;  
 Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TLWGEFQVGGAAAGCGCOTSDNDAAEALNASSKEEALQIIRKIPKYLFOFHNLSNL 60  
 DB 1 TLWGEFQVGGRSARGCGCOTSDNDAAEALNASSKEEALQIIRKIPKYLFOFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 9  
 AAB18686  
 ID AAB18686 standard; peptide; 70 AA.  
 AC AAB18686;  
 XX  
 XX 22-JAN-2001 (first entry)  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 24 /note= "wild type residue replaced with Leu"  
 FT Misc-difference 25 /note= "wild type residue replaced with Leu"  
 FT Misc-difference 26 /note= "wild type residue replaced with Leu"  
 FT  
 XX  
 XX WO200054573-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 XX 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.



PR 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 PA (UYNC-) UNIV NORTH CAROLINA STATE.  
 PI Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 DR Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX  
 PS Claim 52; Page 43-44; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;  
 Query Match 91.4%; Score 331; DB 21; Length 70;  
 Best Local Similarity 91.4%; Pred. No. 3.7e-33;  
 Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDDGAAAGCGQTSNDAAAEALNASSKEEALQIREKIPKYLQFHNLSNL 60  
 DB 1 TLVWGEFQVDDGSGARGCGQTSNDAAAEALNASSKEEALQIAAIPKYLQFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 12  
 AAB18691  
 ID AAB18691 standard; peptide; 70 AA.  
 XX AAB18691;  
 AC AAB18691;  
 XX  
 DT 22-JAN-2001 (first entry)  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 34 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 35 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 36 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 36 /note= "wild type residue replaced with Ala"  
 XX WO200054573-A1.  
 PN 21-SEP-2000.  
 PD

XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 PI WPI; 2000-618851/59.  
 DR Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX  
 PS Disclosure; Page 49; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;  
 Query Match 91.4%; Score 331; DB 21; Length 70;  
 Best Local Similarity 91.4%; Pred. No. 3.7e-33;  
 Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDDGAAAGCGQTSNDAAAEALNASSKEEALQIREKIPKYLQFHNLSNL 60  
 DB 1 TLVWGEFQVDDGSGARGCGQTSNDAAAEALNASSKEEALQIREKIPKYLQFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 13  
 AAB18681  
 ID AAB18681 standard; peptide; 70 AA.  
 XX AAB18681;  
 AC AAB18681;  
 XX  
 DT 22-JAN-2001 (first entry)  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 47 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 48 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 49 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 49 /note= "wild type residue replaced with Ala"  
 XX

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PN WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UUNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 52; Page 44; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 90.6%; Score 328; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 8.8e-33;
XX Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGFQVDGAAAGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
DB 1 TLVWGFQVDGSRAGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 14
AAB18683
AC AAB18683 standard; peptide; 70 AA.
XX AAB18683;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 59 /note= "wild type residue replaced with Ala"
XX Misc-difference 61 /note= "wild type residue replaced with Ala"
XX

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FT Misc-difference 62 /note= "wild type residue replaced with Ala"
XX WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UUNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 53; Page 45; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 90.3%; Score 327; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 1.2e-32;
XX Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGFQVDGAAAGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
DB 1 TLVWGFQVDGSRAGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 AAIFFDKTPEP 70
RESULT 15
AAB18682
ID AAB18682 standard; peptide; 70 AA.
XX AAB18682;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 52

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FT Misc-difference 54 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 55 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 55 /note= "wild type residue replaced with Ala"

WO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYN-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant Al1 protein with a mutation in the Rb binding region  
 PT

XX Claim 53; Page 44-45; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as Al1. Al1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the Al1  
 CC protein are used to produce transgenic plants. The mutation in Al1 is  
 CC present in a ribosome binding region, and expression of mutant Al1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant Al1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA;

Query Match 89.8%; Score 325; DB 21; Length 70;  
 Best Local Similarity 91.4%; Pred. No. 2.1e-32;  
 Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 TLVNGEFQVGGAAAGGCGTSDNDAALNASSKEALQIIREKIPEKYLQFHNLSNL 60  
 Db ||||| : |||||  
 1 TLVNGEFQVGGARGGCGTSDNDAALNASSKEALQIIREKIPEKYLQFHNLSNL 60

OY 61 DRIFDKTPEP 70

Db |||||  
 61 DRIFDKTPEP 70

Search completed: December 23, 2003, 08:56:28  
 Job time : 33.6667 secs







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; MOLECULE TYPE: protein
US-08-838-151A-55

Query Match          59.4%; Score 215; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 2.4e-19;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY      1 TLVGGFQVDGAAAGCGCCTSDNDAAFALNASSKERALQIIRBKIPKYLFOFHNLSNL 60
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Db      110 TIWGGFQVDGSRGARGGQSANDSYAKALNADIESALYILKGEQFDYVLQHHNIRSNL 169
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QY      61 DRIFDKTPEP 70
         :|||:||||
Db      170 ERIFVKVPEP 179
         :|||:||||

RESULT 6
US-08-809-103B-2
; Sequence 2, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-2

Query Match 59.4%; Score 215; DB 3; Length 359;
Best Local Similarity 55.1%; Pred.No. 2.4e-19;
Matches 38; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVWGEFOVDGAAGGCGTNSDAAAEALNASSKEALQITREKTPKYLFPQHNLNSLD 61
Db 111 LEWGTTFIDGRSARGGGQGTANDAYAKINAGSKSQALDVLTKELAPRDYVLHFHINSNLD 170

Qy 62 RIFDKTPEP 70

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Db 171 KVFQVPPAP 179

# RESULT 7

US-08-809-103B-4  
 ; Sequence 4, Application US/08809103B  
 ; Patent No. 6133505  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GRONENBORN, Bruno  
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: YOUNG & THOMPSON  
 ; STREET: 745 South 23rd Street  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; COUNTRY: U.S.A.  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/809,103B  
 ; FILING DATE: 17-MAR-1997  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: FR 94.11040  
 ; FILING DATE: 15-SEP-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/FR95/01192  
 ; FILING DATE: 15-SEP-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: PATCH, Andrew J.  
 ; REGISTRATION NUMBER: 32,925  
 ; REFERENCE/DOCKET NUMBER: US94AL CNR TOM  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 521-2297  
 ; TELEFAX: (703) 685-0573  
 ; TELEX: 248425 EMBON  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 359 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-809-103B-4

Query Match 59.4%; Score 215; DB 3; Length 359;

Best Local Similarity 55.1%; Pred. No. 2.4e-19; Indels 0; Gaps 0;  
 Matches 38; Conservative 12; Mismatches 19;

QY 2 LVWGEFQVDAAGGCOTSDNDAALNASSKEALQIREKIPKYLFOFHNLSNLD 61  
 Db 111 LEWGTFOIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFHNLSNLD 170

QY 62 RIFDKTPEP 70

Db 171 KVFQVPPAP 179

# RESULT 8

US-08-809-103B-6  
 ; Sequence 6, Application US/08809103B  
 ; Patent No. 6133505  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GRONENBORN, Bruno  
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: YOUNG & THOMPSON  
 STREET: 745 South 23rd Street  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/809,103B  
 FILING DATE: 17-MAR-1997  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 94.11040  
 FILING DATE: 15-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/FR95/01192  
 FILING DATE: 15-SEP-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PATCH, Andrew J.  
 REGISTRATION NUMBER: 32,925  
 REFERENCE/DOCKET NUMBER: US94AL CNR TOM  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 521-2297  
 TELEFAX: (703) 685-0573  
 TELEX: 248425 EMBON  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 359 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-809-103B-6

Query Match 59.4%; Score 215; DB 3; Length 359;

Best Local Similarity 55.1%; Pred. No. 2.4e-19; Indels 0; Gaps 0;  
 Matches 38; Conservative 12; Mismatches 19;

QY 2 LVWGEFQVDAAGGCOTSDNDAALNASSKEALQIREKIPKYLFOFHNLSNLD 61  
 Db 111 LEWGTFOIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFHNLSNLD 170

QY 62 RIFDKTPEP 70

Db 171 KVFQVPPAP 179

# RESULT 9

US-08-809-103B-8  
 ; Sequence 8, Application US/08809103B  
 ; Patent No. 6133505  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GRONENBORN, Bruno  
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: YOUNG & THOMPSON  
 ; STREET: 745 South 23rd Street  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; COUNTRY: U.S.A.  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/809,103B

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; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8

Query Match 59.4%; Score 215; DB 3; Length 359;
Best Local Similarity 55.1%; Pred. No. 2.4e-19;
Matches 38; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVMGFEQVDGAAAGCGCQTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSLD 61
Db 111 LEWGTQIDGRSARGGQQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSLD 170

QY 62 RIFDKTPEP 70
Db 171 KVQFVEPPAP 179

RESULT 10
US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match 58.8%; Score 213; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 4.4e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLWVGFEQVDGAAAGCGCQTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNL 60
Db 110 TIWEGDFQIDGRSARGGQQSANDSYAKALNASSVQSALAVLREEQPKDFVLQHNIRSNL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 11
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match 58.8%; Score 213; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 4.4e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLWVGFEQVDGAAAGCGCQTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNL 60
Db 110 TIWEGDFQIDGRSARGGQQSANDSYAKALNASSVQSALAVLREEQPKDFVLQHNIRSNL 169
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Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 12
US-08-838-151A-6
; Sequence 6, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6

Query Match 58.8%; Score 213; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 4.4e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLWGEFQVDGAAAGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
Db 110 TIEWGDFQIDGRSARGGQQSANDSYAKALNASSVQSALAVLRREQPKDFVLQNHINRSL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 13
US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8

Query Match 58.8%; Score 213; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 4.4e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLWGEFQVDGAAAGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
Db 110 TIEWGDFQIDGRSARGGQQSANDSYAKALNASSVQSALAVLRREQPKDFVLQNHINRSL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 14
US-08-838-151A-24
; Sequence 24, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A

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; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8

Query Match 58.8%; Score 213; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 4.4e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLWGEFQVDGAAAGCGCQTSNDAAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
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Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 14
US-08-838-151A-24
; Sequence 24, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A

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; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; US-08-838-151A-24

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Best Local Similarity 62.3%; Pred. No. 2e-17;
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QY 64 F 64
Db 171 F 171

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RESULT 15
US-08-838-151A-27
; Sequence 27, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-27

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds

(without alignments)  
172.015 Million cell updates/sec

Title: US-09-289-346B-2

Perfect score: 362

Sequence: 1 TLVWGFQVDGAAAGGCGT.....FQFHNLNSLDRIFDKTPEP 70

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Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	349	96.4	356	10	US-09-289-346A-11
4	341	94.2	70	10	US-09-289-346A-9
5	338	93.4	70	10	US-09-289-346A-12
6	337	93.1	70	10	US-09-289-346A-16
7	335	92.5	70	10	US-09-289-346A-8
8	335	92.5	70	10	US-09-289-346A-14
9	334	92.3	70	10	US-09-289-346A-10
10	333	92.0	70	10	US-09-289-346A-13
11	331	91.4	70	10	US-09-289-346A-4
12	331	91.4	70	10	US-09-289-346A-15
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15	325	89.8	70	10	US-09-289-346A-6

16	317	87.6	70	10	US-09-289-346A-3
17	69.5	19.2	512	12	US-10-301-661A-4
18	68.5	18.9	1713	15	US-10-171-311-113
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45	57.5	15.9	643	9	US-09-815-242-5394

#### ALIGNMENTS

RESULT 1  
US-09-289-346A-2  
; Sequence 2, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kongs, Ling-jie  
; APPLICANT: Gruijssem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (12)..(15)  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep  
; OTHER INFORMATION: Protein (aa 110-179) with alanine  
; OTHER INFORMATION: replacement (RSAR125->AAAA125).  
US-09-289-346A-2

Query Match 100.0%; Score 362; DB 10; Length 70;  
Best Local Similarity 100.0%; Pred. No. 2.1e-38;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 TLVWGFQVDGAAAGGCGTSDAAAEALNASSKERALQIIRKIPKYLQFQHNLSNL 60  
Qy 61 DRIFDKTPEP 70

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Db      61 DRIFDKTPEP 70
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US-09-289-346A-1
; Sequence 1, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-1

Query Match      96.4%; Score 349; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 9.3e-37;
Matches 67; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 TLVWGEFQVDDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIKEPKYLFQFHNLSNL 60
|||||
Db      1 TLVWGEFQVDDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIKEPKYLFQFHNLSNL 60
|||||
QY      61 DRIFDKTPEP 70
|||||
Db      61 DRIFDKTPEP 70
|||||

RESULT 3
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11

Query Match      96.4%; Score 349; DB 10; Length 356;
Best Local Similarity 95.7%; Pred. No. 8.1e-36;
Matches 67; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 TLVWGEFQVDDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIKEPKYLFQFHNLSNL 60
|||||
Db      1 TLVWGEFQVDDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIKEPKYLFQFHNLSNL 60
|||||
QY      61 DRIFDKTPEP 70
|||||
Db      61 DRIFDKTPEP 70
|||||

RESULT 4
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9

Query Match      94.2%; Score 341; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 9.7e-36;
Matches 66; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 TLVWGEFQVDDGAAAGCGCQTSNDAAAEALNASSKEEALQIIRKIKEPKYLFQFHNLSNL 60
|||||
Db      1 TLVWGEFQVAGRSARGCGCQTSNDAAAEALNASSKEEALQIIRKIKEPKYLFQFHNLSNL 60
|||||
QY      61 DRIFDKTPEP 70
|||||
Db      61 DRIFDKTPEP 70
|||||

RESULT 5
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12

Query Match      93.4%; Score 338; DB 10; Length 70;
```



```
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->AA118).
US-09-289-346A-8

Query Match          92.5%; Score 335; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 5.6e-35;
Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 1 TLVWGEFQVDGRSARGGCAASNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 6
US-09-289-346A-16
; Sequence 16, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-16

Query Match          93.1%; Score 337; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 3.1e-35;
Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 1 TLVWGEFQVDGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 7
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)..(8)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
```

```
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->AA118).
US-09-289-346A-8

Query Match          92.5%; Score 335; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 5.6e-35;
Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 1 TLVWGEAAVDGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 8
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14

Query Match          92.5%; Score 335; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 5.6e-35;
Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 1 TLVWGEFQVDGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 61 DRIFDKTPEP 70
   ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 9
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
```

```
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAA136->LLL136).
US-09-289-346A-10

Query Match          92.3%; Score 334; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 7.5e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGAAAGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 TLVWGFQVDGSRAGCGCQTSNDLLLEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DRIFDKTPEP 70
   |||||:|||||
Db 61 DRIFDKTPEP 70
   |||||:|||||

RESULT 10
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-13

Query Match          92.0%; Score 333; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1e-34;
Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGAAAGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 TLVWGFQVDGSRAGCGCQTSAAAAAEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DRIFDKTPEP 70
   |||||:|||||
Db 61 DRIFDKTPEP 70
   |||||:|||||

RESULT 11
US-09-289-346A-4
; Sequence 4, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
```

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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; NAME/KEY: VARIANT
; LOCATION: (42)..(44)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REK154->AAA154).
US-09-289-346A-4

Query Match          91.4%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.8e-34;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGAAAGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 TLVWGFQVDGSRAGCGCQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DRIFDKTPEP 70
   |||||:|||||
Db 61 DRIFDKTPEP 70
   |||||:|||||

RESULT 12
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match          91.4%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.8e-34;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGAAAGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 TLVWGFQVDGSRAGCGCQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DRIFDKTPEP 70
   |||||:|||||
Db 61 DRIFDKTPEP 70
   |||||:|||||

RESULT 13
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
```

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; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (EKY159->AAA159).
US-09-289-346A-5

Query Match          90.6%; Score 328; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 4.3e-34;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFOVDCAAAAGGCQTGNDAAAEALNASSKEEALQIIREKIPKYLQFHHNLSNL 60
Db 1 TLVWGEFOVDCRSARGGCQTGNDAAAEALNASSKEEALQIIREKIPKYLQFHHNLSNL 60

QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 14
US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (59)..(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDRI72->ALAA172).
US-09-289-346A-7

Query Match          90.3%; Score 327; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 5.8e-34;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFOVDCAAAAGGCQTGNDAAAEALNASSKEEALQIIREKIPKYLQFHHNLSNL 60
Db 1 TLVWGEFOVDCRSARGGCQTGNDAAAEALNASSKEEALQIIREKIPKYLQFHHNLSNL 60

QY 61 DRIFDKTPEP 70
Db 61 AAIFDKTPEP 70

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds  
(without alignments)  
673.181 Million cell updates/sec

Title: US-09-289-346B-2  
Perfect score: 362  
Sequence: 1 TLVWGEFQVDDGAAAGGCGT.....FQHNLNLSNLDRIFDKTPPEP 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	349	96.4	352	1 QOCVLT	Al1 protein - toma
2	249	68.8	361	1 QOCVPT	Al1 protein - toma
3	236	65.2	358	2 S07594	hypothetical prote
4	229	63.3	362	1 JQ1887	Al1 protein - toma
5	222	61.3	359	2 S39211	gene Cl protein -
6	218	60.2	349	2 JQ2300	replicase - pepper
7	218	60.2	349	2 S31875	Al1 protein - pepp
8	215	59.4	359	2 S22593	hypothetical prote
9	212	58.6	351	2 JQ2327	Al1 protein - indi
10	212	58.6	355	1 QOCVW1	Al1 protein - abut
11	209	57.7	358	1 JQ1870	Al1 protein - toma
12	209	57.7	359	2 S39235	gene Cl protein -
13	209	57.7	385	2 S28360	Al1 protein - beet
14	202	55.8	360	2 S59885	replication-associ
15	200	55.2	357	1 QOCVCI	Al1 protein - toma
16	142	39.2	131	2 S45059	Al1 protein (clone
17	124	34.3	347	1 QOCVSI	Al1 protein - squa
18	68.5	18.9	1713	2 A55347	adhesive ligand ep
19	65.5	18.1	1610	2 A46227	voltage-dependent
20	65.5	18.1	1646	2 JH0422	calcium channel al
21	65.5	18.1	2161	2 JH0564	calcium channel al
22	65.5	18.1	2181	2 A38198	voltage-dependent
23	65.5	18.1	2203	2 T42742	alcohol dehydrogen
24	65	18.0	371	2 B69502	probable peptidyl-
25	64.5	17.8	299	2 B71967	glycerol dehydrat
26	64.5	17.8	335	1 DEBSGF	thiolesterase B (E
27	64.5	17.8	557	2 A47162	acetyl-CoA C-acety
28	63.5	17.5	392	2 T45290	probable NADH oxid
29	63	17.4	397	2 B71078	

MG223 homolog F10-  
hypothetical prote  
protein-Npi-phosph  
conserved hypotet  
Cl protein - tobac  
UDP-glucose 4-epim  
CYC1/CYP3 transcri  
probable phosphoe  
iron(III)-binding  
acetyl-CoA C-acety  
Fc gamma (Igg) rec  
hypothetical prote  
probable flagellar  
fructose specific  
E2 protein - human  
CDP-diacylglycerol

30 62.5 17.3 419 2 S73846  
31 62.5 17.3 1033 2 E97700  
32 62 17.1 154 2 AD3475  
33 62 17.1 181 2 G97976  
34 62 17.1 295 2 D42452  
35 62 17.1 308 2 C84072  
36 62 17.1 1502 1 RBYH1  
37 61.5 17.0 481 2 A70091  
38 61 16.9 338 2 AG3582  
39 61 16.9 392 2 T44362  
40 61 16.9 587 2 JC1419  
41 60.5 16.7 136 2 T22440  
42 60.5 16.7 201 2 A81380  
43 60.5 16.7 652 2 E89841  
44 60 16.6 384 1 W2ML41  
45 60 16.6 447 2 S52437

ALIGNMENTS

RESULT 1  
QOCVLT  
Al1 protein - tomato golden mosaic virus  
C:Species: tomato golden mosaic virus  
A:Note: host Nicotiana sp. (tobacco)  
C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Apr-1994  
C:Accession: A04170  
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.  
EMBO J. 3, 2197-2205, 1984  
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat  
A:Reference number: A04163  
A:Accession: A04170  
A:Molecule type: DNA  
A:Residues: 1-352 <HAM>  
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 96.4%; Score 349; DB 1; Length 352;  
Best Local Similarity 95.7%; Pred. No. 1.5e-30;  
Matches 67; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDDGAAAGGCGTSDNDAALNASSKEALQIIRKIPKYLQFPHNLSNL 60  
Db 111 TLVWGEFQVDDGAAAGGCGTSDNDAALNASSKEALQIIRKIPKYLQFPHNLSNL 170

Qy 61 DRIFDKTPPEP 70  
Db 171 DRIFDKTPPEP 180

RESULT 2  
QOCVPT  
Al1 protein - potato yellow mosaic virus (isolate Venezuela)  
C:Species: potato yellow mosaic virus  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jun-2000  
C:Accession: J00364  
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.  
J. Gen. Virol. 72, 1515-1520, 1991  
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel  
A:Reference number: J00362; MUID:91311403; PMID:1856690  
A:Accession: J00364  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-361 <COU>  
A:Cross-references: GB:D00940; NID:g222458; PIDN:BAA00782.1; PID:g222459  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 68.8%; Score 249; DB 1; Length 361;  
Best Local Similarity 66.7%; Pred. No. 1.4e-13;  
Matches 46; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60  
Db 110 TLVWGEFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60  
Qy 61 DRIFDKTPEP 69  
Db 170 DRIFDKTPEP 178

RESULT 3  
S07594  
hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)  
C;Species: cassava latent virus  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Sep-1999  
C;Accession: S07594  
R;Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.  
Nucleic Acids Res. 18, 197-198, 1990  
A;Title: Nucleotide sequence of the infectious cloned DNA components of African cassava  
A;Reference number: S07590; MUID:90174930; PMID:2308831  
A;Accession: S07594  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-358 <MOR>  
A;Cross-references: EMBL:X17095; NID:959371; PIDN:CAA34953.1; PID:959376  
C;Genetics:  
A;Map position: segment DNAL  
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 65.2%; Score 236; DB 2; Length 358;  
Best Local Similarity 60.0%; Pred. No. 3.6e-18;  
Matches 42; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60  
Db 109 TVEWGEFQIDGRSARGGQQTANDAYAKALNSGKSEALNVIKELAPRDYILFHNLNSNL 168

Qy 61 DRIFDKTPEP 70  
Db 169 DRIFDKTPEP 178

RESULT 4  
JQ1887  
AL1 protein - tomato yellow leaf curl virus (strain Australia)  
N;Alternate names: CI protein  
C;Species: tomato yellow leaf curl virus  
C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 07-May-1999  
C;Accession: JQ1887  
R;Dry, I.B.; Rigen, J.E.; Krake, L.R.; Mullineaux, P.M.; Rezaian, M.A.  
J. Gen. Virol. 74, 147-151, 1993  
A;Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.  
A;Reference number: JQ1885; MUID:93139778; PMID:8423446  
A;Accession: JQ1887  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-362 <DRY>  
A;Cross-references: GB:S53251  
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 63.3%; Score 229; DB 1; Length 362;  
Best Local Similarity 52.9%; Pred. No. 2.1e-17;  
Matches 45; Conservative 10; Mismatches 14; Indels 16; Gaps 1;

Qy 1 TLVWGEFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60  
Db 110 TLEWGEFQIDGRSARGGQQTANDAYAKALNSGKSEALNVIKELAPRDYILFHNLNSNL 169

Qy 61 DRI-----FDKTPPE 69  
Db 110 TLEWGEFQIDGRSARGGQQTANDAYAKALNSGKSEALNVIKELAPRDYILFHNLNSNL 169

Query Match 60.2%; Score 218; DB 2; Length 349;  
Best Local Similarity 57.1%; Pred. No. 3.3e-16;  
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60  
Db 110 TVEWGEFQIDGRSARGGQQTANDAYAKALNSGKSEALNVIKELAPRDYILFHNLNSNL 169

Qy 61 DRIFDKTPEP 70  
Db 170 NRIFQTPPEP 179

RESULT 7  
S31875  
AL1 protein - pepper rizado amarillo virus  
C;Species: pepper rizado amarillo virus  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 20-Sep-1999  
C;Accession: S31875  
R;Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera-I  
submitted to the EMBL Data Library, February 1993  
A;Description: Complete nucleotide sequence of pepper huasteco virus: analysis and com  
A;Reference number: S31872

Db 170 DRIFDKTPEP 178

RESULT 5  
S39211  
gene C1 protein - tomato yellow leaf curl virus  
C;Species: tomato yellow leaf curl virus  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Sep-1999  
C;Accession: S39211  
R;Noris, E.; Hidalgo, E.; Accotto, G.; Moriones, E.  
submitted to the EMBL Data Library, August 1993  
A;Description: High similarity among the tomato yellow leaf curl virus isolates from t  
A;Reference number: S39209  
A;Accession: S39211  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-359 <NOR>  
A;Cross-references: EMBL:Z25751; NID:9433655; PIDN:CAA81026.1; PID:9433658  
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 61.3%; Score 222; DB 2; Length 359;  
Best Local Similarity 58.0%; Pred. No. 1.2e-16;  
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVWGEFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 61  
Db 111 LEWGTFTQIDGRSARGGQQTANDAYAKALNSGKSEALNVIKELAPRDYILFHNLNSNL 170

Qy 62 RIFDKTPEP 70  
Db 171 RVFQTPPEP 179

RESULT 6  
JQ2300  
replicase - pepper huasteco virus (component A)  
N;Alternate names: ORF AL1 protein  
C;Species: pepper huasteco virus  
C;Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 20-Sep-1999  
C;Accession: JQ2300  
R;Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Herrera-Estrella, L.; Rivera-Bustamante, R.  
J. Gen. Virol. 74, 2225-2231, 1993  
A;Title: Complete nucleotide of pepper huasteco virus: Analysis and comparison with b  
A;Reference number: JQ2299; MUID:94015007; PMID:8409944  
A;Accession: JQ2300  
A;Molecule type: DNA  
A;Residues: 1-349 <TOR>  
A;Cross-references: GB:X70418; NID:961023; PIDN:CAA49856.1; PID:961025  
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 60.2%; Score 218; DB 2; Length 349;  
Best Local Similarity 57.1%; Pred. No. 3.3e-16;  
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60  
Db 110 TVEWGEFQIDGRSARGGQQTANDAYAKALNSGKSEALNVIKELAPRDYILFHNLNSNL 169

Qy 61 DRIFDKTPEP 70  
Db 170 NRIFQTPPEP 179

RESULT 7  
S31875  
AL1 protein - pepper rizado amarillo virus  
C;Species: pepper rizado amarillo virus  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 20-Sep-1999  
C;Accession: S31875  
R;Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera-I  
submitted to the EMBL Data Library, February 1993  
A;Description: Complete nucleotide sequence of pepper huasteco virus: analysis and com  
A;Reference number: S31872

A:Accession: S31875  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <TOR>  
A:Cross-references: EMBL:X70418; NID:g61023; PIDN:CAA49856.1; PID:g61025  
A>Note: the source is designated as pepper huasteco virus  
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 60.2%; Score 218; DB 2; Length 349;  
Best Local Similarity 57.1%; Pred. No. 3.3e-16;  
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFVDGAAAGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60  
Db 110 TVEWGEFQIDGRSARGGQGSANDTYAKALNSASAEALQIIRKEQFQHFFLOFHNIVNSA 169

Qy 61 DRIFDKTPEP 70  
Db 170 NRIFQTPPEP 179

## RESULT 8

S22593  
hypothetical protein C4 - tomato yellow leaf curl virus  
C:Species: tomato yellow leaf curl virus  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Sep-1999  
C:Accession: S22593  
R:Khayr-Pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.  
Nucleic Acids Res. 19, 6763-6769, 1991  
A:Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite  
A:Reference number: S22598; MUID:92107660; PMID:1840676  
A:Accession: S22593  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-359 <KHE>  
A:Cross-references: EMBL:X61153; NID:G62211; PIDN:CAA43466.1; PID:G62217  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991  
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.4%; Score 215; DB 2; Length 359;  
Best Local Similarity 55.1%; Pred. No. 7.2e-16;  
Matches 38; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVWGEFVDGAAAGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLD 61  
Db 111 LEWTFQIDGRSARGGQGTANDAYAKALNAGSKSQALDVIRELAPRDYVLFHFNINSNLD 170

Qy 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

## RESULT 9

JQ2327  
AL1 protein - Indian cassava mosaic virus  
N:Alternate names: replication-associated protein  
C:Species: Indian cassava mosaic virus  
C:Date: 28-Aug-1995 #sequence\_revision 07-Oct-1994 #text\_change 20-Sep-1999  
C:Accession: JQ2327; S35883  
R:Hong, Y.G.; Robinson, D.J.; Harrison, B.D.  
J. Gen. Virol. 74, 2437-2443, 1993  
A:Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-transmitted cassava mosaic viruses  
A:Reference number: JQ2326; MUID:94065670; PMID:8245859  
A:Accession: JQ2327  
A:Molecule type: DNA  
A:Residues: 1-351 <HON>  
A:Cross-references: EMBL:Z24758; NID:G395351; PIDN:CAA80891.1; PID:G584046  
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 58.6%; Score 212; DB 2; Length 351;  
Best Local Similarity 53.7%; Pred. No. 1.5e-15;  
Matches 40; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 4 WGEFQVDGAAAGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63  
Db 113 WGTFOIDGRSARGGQGSANDAYAAALNSGSKSEALKILRELAAPRDYLRDFHFISSNLDRI 172

Qy 64 FDKTPEP 70  
Db 173 FTKPPPP 179

## RESULT 10

QOCVWI  
AV1 protein - abutilon mosaic virus (isolate West India)  
C:Species: abutilon mosaic virus  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 08-Apr-1994  
C:Accession: A36214  
R:Frischmuth, T.; Zimmatt, G.; Jeske, H.  
Virology 178, 461-468, 1990  
A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as w  
A:Reference number: A36214; MUID:91020984; PMID:2219703  
A:Accession: A36214  
A:Molecule type: DNA  
A:Residues: 1-355 <FRI>  
A:Cross-references: EMBL:X15983  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 58.6%; Score 212; DB 1; Length 355;  
Best Local Similarity 55.7%; Pred. No. 1.5e-15;  
Matches 39; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60  
Db 110 TAEWGEFQIDGRSARGGQGTANDSYAKALNAGDVQSALNILEQPKDYVLQNHINSNL 169

Qy 61 DRIFDKTPEP 70  
Db 170 ERIFAKAPEP 179

## RESULT 11

JQ1870  
AL1 protein - tomato mottle virus (isolate Florida)  
C:Species: tomato mottle virus  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 07-May-1999  
C:Accession: JQ1870  
R:Abouzid, A.M.; Polston, J.E.; Hiebert, E.  
J. Gen. Virol. 73, 3225-3229, 1992  
A:Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated fr  
A:Reference number: JQ1869; MUID:93107858; PMID:1469361  
A:Accession: JQ1870  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-358 <ABO>  
A:Cross-references: GB:L14460  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 57.7%; Score 209; DB 1; Length 358;  
Best Local Similarity 52.9%; Pred. No. 3.3e-15;  
Matches 37; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60  
Db 107 TIWGEFQIDGRSARGGQGSANDSYAKALNAGSVQSALAVLREQPKDFVLQNHINSNL 166

Qy 61 DRIFDKTPEP 70  
Db 167 ERIFAKAPEP 176

## RESULT 12

S39235  
gene C1 protein - tomato yellow leaf curl virus  
C/Species: tomato yellow leaf curl virus  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Sep-1997  
C/Accession: S39235  
R/Crespi, S.; Norris, E.; Vaira, A.; Bosco, D.; Accotto, G.  
submitted to the EMBL Data Library, December 1993  
A/Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.  
A/Reference number: S39233  
A/Accession: S39235  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-359 <CRE>  
A/Cross-references: EMBL:Z28390; NID:g1041671; PID:g1334964  
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 57.7%; Score 209; DB 2; Length 359;  
Best Local Similarity 53.6%; Pred. No. 3.3e-15;  
Matches 37; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVMGEFQVDGAAAGGCOTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLD 61  
Db 111 LEWTFQIDGRSARGGQQTANDAYAKALNARSKEALDVIKQLAPRDYVLHFHNSNLD 170

Qy 62 RIFDKTPEP 70  
Db 171 KVQVPPAP 179

RESULT 13  
S28360  
AL1 protein - beet curly top virus  
C/Species: beet curly top virus  
C/Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Sep-1999  
C/Accession: S28360  
R/Stanley, J.; Markham, P.G.; Callis, R.J.; Pinner, M.S.  
EMBO J. 5, 1761-1767, 1986  
A/Title: The nucleotide sequence of an infectious clone of the geminivirus beet curly top  
A/Reference number: S28360  
A/Accession: S28360  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-385 <STA>  
A/Cross-references: GB:M24597; EMBL:X04144; NID:g210678; PID:AAA42751.1; PID:g210679  
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 57.7%; Score 209; DB 2; Length 385;  
Best Local Similarity 52.9%; Pred. No. 3.5e-15;  
Matches 37; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGGCOTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60  
Db 137 TIWGEFQIDGRSARGGQQTANDSYAKALNATSLDQALQILKEQPKDYFLQHNLLNNA 196

Qy 61 DRIFDKTPEP 70  
Db 197 QKIFQRPDP 206

RESULT 14  
S59885  
replication-associated protein C1 - tomato yellow leaf curl virus  
C/Species: tomato yellow leaf curl virus  
C/Date: 14-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 20-Sep-1999  
C/Accession: S59885  
R/Hong, Y.; Harrison, B.D.  
submitted to the EMBL Data Library, February 1995  
A/Description: Nucleotide sequences from tomato leaf curl viruses from different countries  
geminiviruses.  
A/Reference number: S58346  
A/Accession: S59885  
A/Status: preliminary  
A/Molecule type: DNA

A/Residues: 1-360 <HON>  
A/Cross-references: EMBL:Z48182; NID:g944836; PIDN:CAA88229.1; PID:g974211  
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 55.8%; Score 202; DB 2; Length 360;  
Best Local Similarity 57.6%; Pred. No. 1.9e-14;  
Matches 38; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 4 WGEFQVDGAAAGGCOTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63  
Db 113 FGVFQIDGRSARGGQQSANDAYAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 172

Qy 64 FDKTPE 69  
Db 173 FTPSAE 178

RESULT 15  
QOCVC1  
AL1 protein - tomato yellow leaf curl virus  
N/Alternate names: C1 protein  
C/Species: tomato yellow leaf curl virus  
C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
C/Accession: D40779  
R/Navot, N.; Fichersky, E.; Zeidan, M.; Zamir, D.; Czoenek, H.  
Virology 185, 151-161, 1991  
A/Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single  
A/Reference number: A40779; MUID:92024070; PMID:1926771  
A/Accession: D40779  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-357 <NAV>  
A/Cross-references: GB:X15656; NID:g62204; PIDN:CAA33688.1; PID:g62207  
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 55.2%; Score 200; DB 1; Length 357;  
Best Local Similarity 62.3%; Pred. No. 3.1e-14;  
Matches 38; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 4 WGEFQVDGAAAGGCOTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63  
Db 111 FGVFQIDGRSARGGQQSANDAYAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 170

Qy 64 F 64  
Db 171 F 171

Search completed: December 23, 2003, 09:05:17  
Job time : 12 secs

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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds  
(without alignments)  
569.747 Million cell updates/sec

Title: US-09-289-346B-2

Perfect score: 382

Sequence: 1 TLVWGEFQVDGAAAGGCQT.....FQFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	349	96.4	352	1	VAL1	TGMV	P03567 tomato gold
2	249	68.8	361	1	VAL1	PYMWV	P27258 potato yell
3	236	65.2	358	1	VAL1	CLVX	P14982 cassava lat
4	236	65.2	358	1	VAL1	CLVN	P14972 cassava lat
5	229	63.3	362	1	VAL1	TYLCA	P36279 tomato yell
6	222	61.3	359	1	VAL1	TYLCU	P38609 tomato yell
7	218	60.2	349	1	VAL1	PHUV	P06923 pepper huas
8	215	59.4	359	1	VAL1	TYLCM	P27260 tomato yell
9	213	58.8	353	1	VAL1	BGMV	P05175 bean golden
10	212	58.6	355	1	VAL1	ABMVW	P1947 abutilon mo
11	209	57.7	358	1	VAL1	BCTV	P14991 beet curly
12	209	57.7	361	1	VAL1	TMOV	P06657 tomato mott
13	200	55.2	357	1	VAL1	TYLCV	P27259 tomato yell
14	124	34.3	347	1	VAL1	SLCV	P29048 squash leaf
15	68.5	18.9	1713	1	LM43	HUMAN	O16787 homo sapien
16	67	18.5	298	1	OLG2	CHICK	Q30XB3 gallus gall
17	65.5	18.1	1610	1	CCAD	MESAU	Q39244 mesocricetu
18	65.5	18.1	2161	1	CCAD	HUMAN	Q01668 homo sapien
19	65.5	18.1	2203	1	CCAD	RAT	P27732 rattus norv
20	64.5	17.8	299	1	Y175	HELPIJ	Q9ZMG7 helicobacte
21	64.5	17.8	334	1	G3P	BACST	P00362 bacillus st
22	64.5	17.8	335	1	G3P	BACCO	P15115 bacillus co
23	64.5	17.8	557	1	SNSE	ANAPL	Q04791 anas platyr
24	62.5	17.3	419	1	Y223	MYCPN	P75465 mycoplasma
25	62	17.1	295	1	VAL1	TYDVA	P31617 tobacco vel
26	62	17.1	1502	1	CYP1	YEAST	P12351 saccharomyc
27	60.5	16.7	136	1	Y452	CABEL	O62250 caenorhabdi
28	60	16.6	387	1	VE2	HPV41	P27552 human papil
29	60	16.6	447	1	CDS4	DROME	P56079 d phosphati
30	60	16.6	513	1	HEMO	CHICK	P18080 gallus gall
31	59.5	16.4	863	1	AMPN	CAUCR	P37893 caulobacter
32	59	16.3	129	1	RK12	PORPU	P51339 porphyra pu
33	59	16.3	247	1	YCP4	YEAST	P25349 saccharomyc

34 58.5 16.2 299 1 Y175\_HELPIY P56112 helicobacte  
35 58.5 16.2 439 1 XYLA\_LACIA Q9CF97 lactococcus  
36 58.5 16.2 491 1 AMPA\_ANASP Q82064 anabaena sp  
37 58.5 16.2 589 1 Y567\_HAEIN P45221 haemophilus  
38 58.5 16.2 1044 1 BUB1\_SCHPO O94751 schizosach  
39 58.5 16.2 2190 1 CCAD\_CHICK O73700 gallus gall  
40 58 16.0 387 1 Y4PF\_RHISN P55615 rhizobium s  
41 58 16.0 422 1 BCHN\_ACTIRU Q9WXB4 acidiphilia  
42 58 16.0 617 1 YACH\_ECOLI P36682 escherichia  
43 58 16.0 640 1 DNAC\_RHOMR O9XCB1 rhodothermu  
44 58 16.0 874 1 SLAP\_BACLI P49052 bacillus li  
45 57.5 15.9 266 1 ETFB\_MYCLE O33095 mycobacteri

#### ALIGNMENTS

RESULT 1  
ID VAL1 TGMV STANDARD; PRT; 352 AA.  
AC P03567;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE AL1 protein.  
GN AC1.  
OS Tomato golden mosaic virus (TGMV).  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=10831;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;  
RT \*Complete nucleotide sequence of the infectious cloned DNA components  
RT of tomato golden mosaic virus: potential coding regions and regulatory  
RT sequences.";  
RL EMBL J. 3:2197-2205(1984).  
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.  
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CC -----  
DR EMBL; K02029; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A04170; Q0CVL1.  
DR InterPro; IPR001191; Gemini\_AL1.  
DR Pfam; PF00799; Gemini\_AL1; 1.  
DR PRINTS; PR00227; GEMCOAT1.  
DR ProDom; PD000736; Gemini\_AL1; 1.  
KW ATP-binding.  
FT NP BIND. 223 230 ATP (POTENTIAL).  
SQ SEQUENCE 352 AA; 40332 MW; C33C93859644B4A4 CRC64;  
Query Match 96.4%; Score 349; DB 1; Length 352;  
Best Local Similarity 95.7%; Pred. No. 2.3e-31;  
Matches 67; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 TLVWGEFQVDGAAAGGCQTSNDAAAEALNASSKEALQIIREKIPKYLQFQFHNLNSL 60  
Db 111 TLVWGEFQVDGRSARGCQTSNDAAAEALNASSKEALQIIREKIPKYLQFQFHNLNSL 170  
Qy 61 DRIFDKTPEP 70  
Db 171 DRIFDKTPEP 180  
RESULT 2  
VAL1 PYMWV STANDARD; PRT; 361 AA.  
ID VAL1 PYMWV  
AC P27258;



```

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE All protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus.";
RL J. Gen. Virol. 72:1515-1520(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
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CC -----
DR EMBL; D00940; BAA00782.1; -.
DR PIR; J00364; QOCVPT.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;

Query Match
Best Local Similarity 68.8%; Score 249; DB 1; Length 361;
Matches 46; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLWGFQVDGAAAGCGCOTSDNDAALNASSKEALQIRKIPKYLQFPHNLSNL 60
DQ 110 TIEWGLFQIDGRSARGGQQTWVDAALNASSKEALQIRKIPKYLQFPHNLSNL 169
QY 61 DRIFDKTPEP 69
DB 170 DRIFDKAPE 178

RESULT 3
VALI CLVK
ID VALI CLVK STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE All protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain West Kenya 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
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CC EMBL; J02057; -: NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E75EB92D69 CRC64;

Query Match
Best Local Similarity 65.2%; Score 236; DB 1; Length 358;
Matches 42; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLWGFQVDGAAAGCGCOTSDNDAALNASSKEALQIRKIPKYLQFPHNLSNL 60
DQ 109 TVEWGQFQIDGRSARGGQGSANDAYAKALNSGSKSEALNVIRELVKDFVLQFPHNLSNL 168
QY 61 DRIFDKTPEP 70
DB 169 DRIFQPPAP 178

RESULT 4
VALI CLVN
ID VALI CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE All protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
RL Nucleic Acids Res. 18:197-198(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
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CC -----
DR EMBL; X17095; CAA34953.1; -.
DR PIR; S07594; S07594.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16B80CB2D5E2C CRC64;

Query Match
Best Local Similarity 65.2%; Score 236; DB 1; Length 358;
Matches 42; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLWGFQVDGAAAGCGCOTSDNDAALNASSKEALQIRKIPKYLQFPHNLSNL 60
DQ 109 TVEWGQFQIDGRSARGGQGSANDAYAKALNSGSKSEALNVIRELVKDFVLQFPHNLSNL 168
QY 61 DRIFDKTPEP 70
DB 169 DRIFQPPAP 178

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RESULT 5
VAL1_TYLCU
ID VAL1_TYLCU STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36447;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93139778; PubMed=8423446;
RT Dry I.B., Rigden J.E., Krake L.R., Mullineaux P.M., Rezaian M.A.;
RA "Nucleotide sequence and genome organization of tomato leaf curl
RT geminivirus.";
RL J. Gen. Virol. 74:147-151(1993).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;

Query Match 63.3%; Score 229; DB 1; Length 362;
Best Local Similarity 52.9%; Pred. No. 4.9e-18;
Matches 45; Conservative 10; Mismatches 14; Indels 16; Gaps 1;

Qy 1 TLVWGFQVDGAAAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLQFHNLSNLD 60
Db 110 TLEWGFQIDGRSARGGQSANDAYAQALNTGSKSEALNVRELAPDYVLFQFHNLSNLD 169

Qy 61 DRI-----FKPTPE 69
Db 170 DRIPTPLEVTVVSPFLSSSFDRVPE 194

RESULT 6
VAL1_TYLCU
ID VAL1_TYLCU STANDARD; PRT; 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Noris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
RT from the west Mediterranean basin: the nucleotide sequence of an
RT infectious clone from Spain.";
RL Arch. Virol. 135:165-170(1994).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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Query Match 60.2%; Score 218; DB 1; Length 349;
Best Local Similarity 57.1%; Pred. No. 7.9e-17;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDGAAAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLQFHNLSNLD 60
Db 110 TLEWGFQIDGRSARGGQSANDYAKALNASSAEALQIREEQHPFLQFHNIVNSA 169

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CC EMBL; Z25751; CAA81026.1; -.
DR PIR; S39211; S39211.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3EC CRC64;

Query Match 61.3%; Score 222; DB 1; Length 359;
Best Local Similarity 58.0%; Pred. No. 2.9e-17;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVWGFQVDGAAAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLQFHNLSNLD 61
Db 111 LEWGFQIDGRSARGGQQTANDAYAKAINAGSKSEALDVIRELAPRDYILHFNHNSLD 170

Qy 62 RIFDKTPEP 70
Db 171 RVFQVPPAP 179

RESULT 7
VAL1_PHVU
ID VAL1_PHVU STANDARD; PRT; 349 AA.
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AL1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
RT comparison with bipartite geminiviruses.";
RL J. Gen. Virol. 74:2225-2231(1993).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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EMBL; X70418; CAA49856.1; -.
DR PIR; JQ2300; JQ2300.
DR PIR; S31875; S31875.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 39722 MW; D5F4E76CD56370F4 CRC64;

Query Match 60.2%; Score 218; DB 1; Length 349;
Best Local Similarity 57.1%; Pred. No. 7.9e-17;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDGAAAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLQFHNLSNLD 60
Db 110 TLEWGFQIDGRSARGGQSANDYAKALNASSAEALQIREEQHPFLQFHNIVNSA 169

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QY 61 DRIFDKTPEP 70
Db 170 NRIFQTPPEP 179

RESULT 8
ID VAL1_TYLCM STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92107660; PubMed=1840676;
RA Kheyt-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
RA Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a
RT whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; M10070; AAA46318.1; --
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 58.4%; Score 213; DB 1; Length 353;
Best Local Similarity 57.1%; Pred. No. 2.9e-16;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGAAAGGCGTSDNAAAEALNASSKEALQIIREKIPEKYLQPHNLNSNL 60
Db 110 TIWGFQVDGSRARGGQSANDSYAKALNADSIESTILKEEPKDYVLQHNIRSNL 169
QY 61 DRIFDKTPEP 70
Db 170 NRIFQTPPEP 179

RESULT 10
ID VAL1_ABMVW STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimrat G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; X15983; --; NOT_ANNOTATED_CDS.
DR PIR; A36214; QOCVW1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
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FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 355 AA; 40257 MW; 16A2CA8A63251E95 CRC64;

Query Match 58.6%; Score 212; DB 1; Length 355;
Best Local Similarity 55.7%; Pred. No. 3.7e-16;
Matches 39; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGTSDNDAAAEALNASSKEEALQIREKIPKYLQFPHNLNSNL 60
Db 110 TLWGEFQIDGRSARGGQQTANDSYAKALNAGDVQSAVNILKEEQPKDYVLQNHNLNSNL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 11
VAL1 ECTV
ID VAL1 BCTV STANDARD; PRT; 358 AA.
AC P14991;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein (40.8 kDa protein).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
RT beet curly top virus."
RL EMBO J. 5:1761-1767 (1986).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
CC EMBL; L14460; AAC32414.1; -
CC PIR; JQ1870; JQ1870.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATL1.
CC ProDom; PD000736; Gemini_AL1; 1.
CC KX ATP-binding.
KW NP_BIND 222 229 ATP (BY SIMILARITY).
FT NP_BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 8138B65CEAC6950 CRC64;

Query Match 57.7%; Score 209; DB 1; Length 361;
Best Local Similarity 52.9%; Pred. No. 8.1e-16;
Matches 37; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGGCGTSDNDAAAEALNASSKEEALQIREKIPKYLQFPHNLNSNL 60
Db 110 TLWGEFQIDGRSARGGQQTANDSYAKALNAGDVQSAVNILKEEQPKDYVLQNHNLNSNL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 13
VAL1 TYLCV
ID VAL1 TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (CI protein).
GN Cl.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component."
RL Virology 185:151-161 (1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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DR EMBL; X15656; CAA33688.1; -.
DR PIR; D40779; QQCVC1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1.1.
KW ATP-binding.
FT NP BIND 219 226 ATP (POTENTIAL).
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match 55.2%; Score 200; DB 1; Length 357;
Best Local Similarity 62.3%; Pred. No. 8e-15;
Matches 38; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 4 WGEFQVDAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNLDRI 63
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
111 FGVSQIDGRGARGQSQANDAYAEALNAGSGSKSEALNLIKAKPKDYTLQFPHNLSSNLDRI 170

QY 64 F 64
Db 171 F 171

RESULT 14
VAL1 SLCV STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE A11 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9108249; PubMed=1984668;
RA Lazarowitz S.G.; Lazdins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype.";
RL Virology 180:58-69(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; M38183; AAC32410.1; ALT_INIT.
DR PIR; C36785; QQCVS1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1.1.
KW ATP-binding.
FT NP BIND 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDAEDDE122110E CRC64;

Query Match 34.3%; Score 124; DB 1; Length 347;
Best Local Similarity 37.9%; Pred. No. 2.1e-06;
Matches 25; Conservative 14; Mismatches 23; Indels 4; Gaps 1;

QY 5 GEFQVDAAGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNLDRI 64
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 GOYKVSQ-----GSKSNKDDVYHNAVAGSAGEALDIKAGDPKTFVYNYHLLANVERLF 171

QY 65 DKTPPEP 70
Db 172 QKPEP 177

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## RESULT 15

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LMA3 HUMAN STANDARD; PRT; 1713 AA.
AC O16787; Q13679; Q13680;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Laminin alpha-3 chain precursor (Epiligrin 170 kDa subunit) (E170)
DE Laminin alpha-3 chain precursor (Epiligrin 170 kDa subunit) (E170)
DE Laminin alpha subunit.
GN LAMA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Keratinocytes;
RX MEDLINE=94357926; PubMed=8077230;
RA Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.;
RT "Cloning of the Lama3 gene encoding the alpha 3 chain of the adhesive
RT ligand epiligrin. Expression in wound repair.";
RL J. Biol. Chem. 269:22779-22787(1994).
RN [2]
RP SEQUENCE OF 1-1331 FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=96163880; PubMed=8586427;
RA Vidal F., Baudoin C., Miguel C., Galliano M.-F., Christiano A.M.,
RA Utito J., Ortonne J.-P., Meneguzzi G.;
RT "Cloning of the laminin alpha 3 chain gene (LAMA3) and identification
RT of a homozygous deletion in a patient with Herlitz junctional
RT epidermolysis bullosa.";
RL Genomics 30:273-280(1995).
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -1- FUNCTION: LAMININ-5 IS THOUGHT TO BE INVOLVED IN (1) CELL ADHESION
CC VIA INTEGRIN ALPHA-3/BETA-1 IN FOCAL ADHESION AND INTEGRIN ALPHA-
CC 6/BETA-4 IN HEMIDESMOSOMES, (2) SIGNAL TRANSDUCTION VIA TYROSINE
CC PHOSPHORYLATION OF PPL25-FAK AND P80, (3) DIFFERENTIATION OF
CC KERATINOCYTES.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The alpha-3 chain is a subunit of laminin-5
CC (epiligrin/kalinin/nicein), and possibly also a component of
CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC MEMBRANES (MAJOR COMPONENT).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=Q16787-1; Sequence=Displayed;
CC Name=B;
CC IsoId=Q16787-2; Sequence=VSP_003037;
CC Note=Sequence incomplete;
CC -1- TISSUE SPECIFICITY: SKIN; RESPIRATORY, URINARY, AND DIGESTIVE
CC EPITHELIA AND IN OTHER SPECIALIZED TISSUES WITH PROMINENT
CC SECRETORY OR PROTECTIVE FUNCTIONS. EPITHELIAL BASEMENT MEMBRANE,
CC AND EPITHELIAL CELL TONGUE THAT MIGRATES INTO A WOUND BED. A
CC DIFFERENTIAL AND FOCAL EXPRESSION OF THE ALPHA-3 CHAIN IS OBSERVED
CC IN THE CNS.
CC -1- INDUCTION: LAMININ-5 IS UP-REGULATED IN WOUND SITES OF HUMAN SKIN.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- DOMAIN: DOMAIN G IS GLOBULAR.
CC -1- DISEASE: DEFECTS IN LAMA3 ARE A CAUSE OF JUNCTIONAL EPIDERMOLYSIS
CC BULLOSA (JEB) GRAVIS, ALSO KNOWN AS HERLITZ TYPE JEB. IT IS A
CC BLISTERING DISORDER IN SKIN THAT IS CHARACTERIZED BY A SEPARATION
CC OF BASAL CELLS FROM THE BASEMENT MEMBRANE DUE TO A DECREASED
CC NUMBER OF HEMIDESMOSOMES. LAMININ-5 IS MISSING FROM THE BASEMENT

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CC MEMBRANE OF PATIENTS WITH THE GRAVIS FORM OF EPIDERMOLYSIS  
 CC BULLOSA.  
 CC -!- SIMILARITY: Contains 3 laminin EGF-like domains.  
 CC -!- SIMILARITY: Contains 5 laminin G-like domains.  
 CC -----  
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 CC -----  
 CC EMBL; L34155; AA59483.1; -;  
 CC EMBL; X85107; CAAS9428.1; -;  
 CC EMBL; X85108; CAAS9429.1; -;  
 CC PIR; A55347; A55347.  
 CC HSP; P02468; ITRF.  
 CC Genew; HGNC:6483; LAMA3.  
 CC MIM; 600805; -;  
 CC MIM; 226700; -;  
 CC GO; GO:0005604; C:basement membrane; TAS.  
 CC GO; GO:0008544; P:epidermal differentiation; TAS.  
 CC InterPro; IPR006209; EGF like.  
 CC InterPro; IPR002049; Laminin EGF.  
 CC InterPro; IPR001791; Laminin G.  
 CC Pfam; PF00053; laminin\_EGF; 2.  
 CC Pfam; PF00054; laminin\_G; 2.  
 CC SMART; SM00180; EGF\_Lam; 2.  
 CC SMART; SM00282; LamG; 5.  
 CC PROSITE; PS00022; EGF 1; 1.  
 CC PROSITE; PS01186; EGF 2; 1.  
 CC PROSITE; PS01248; LAMININ TYPE EGF; 2.  
 CC PROSITE; PS50025; LAM\_G\_DOMAIN; 5.  
 CC KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
 CC Laminin EGF-like domain; Cell adhesion; Repeat; Signal;  
 CC Alternative splicing; Epidermolysis bullosa.  
 CC SIGNAL 1 20 POTENTIAL  
 CC CHAIN 21 1713 LAMININ ALPHA-3 CHAIN.  
 CC DOMAIN 46 201 DOMAIN III A.  
 CC DOMAIN 67 113 LAMININ EGF-LIKE 1.  
 CC DOMAIN 114 166 LAMININ EGF-LIKE 2.  
 CC DOMAIN 167 185 LAMININ EGF-LIKE 3 (INCOMPLETE).  
 CC DOMAIN 186 769 DOMAIN II AND I.  
 CC DOMAIN 770 971 LAMININ G-LIKE 1.  
 CC DOMAIN 978 1140 LAMININ G-LIKE 2.  
 CC DOMAIN 1147 1307 LAMININ G-LIKE 3.  
 CC DOMAIN 1366 1530 LAMININ G-LIKE 4.  
 CC DOMAIN 1537 1710 LAMININ G-LIKE 5.  
 CC DOMAIN 231 327 COILED COIL (POTENTIAL).  
 CC DOMAIN 396 548 COILED COIL (POTENTIAL).  
 CC DOMAIN 594 621 COILED COIL (POTENTIAL).  
 CC DOMAIN 702 785 COILED COIL (POTENTIAL).  
 CC DOMAIN 1686 1713 COILED COIL (POTENTIAL).  
 CC DISULFID 67 76 BY SIMILARITY.  
 CC DISULFID 69 83 BY SIMILARITY.  
 CC DISULFID 86 95 BY SIMILARITY.  
 CC DISULFID 98 111 BY SIMILARITY.  
 CC DISULFID 114 126 BY SIMILARITY.  
 CC DISULFID 116 135 BY SIMILARITY.  
 CC DISULFID 137 146 BY SIMILARITY.  
 CC DISULFID 149 164 BY SIMILARITY.  
 CC DISULFID 202 202 INTERCHAIN (PROBABLE).  
 CC DISULFID 205 205 INTERCHAIN (PROBABLE).  
 CC SITE 658 660 CELL ATTACHMENT SITE (POTENTIAL).  
 CC CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 645 645 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 882 882 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 964 964 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 1108 1108 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 1131 1131 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 1325 1325 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1477 1477 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1667 1667 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 1 45 MGNLWTFGAALGCGCLGYSSQQQRVPFLQPPGSQLQASYVE  
 FT FRPS -> KVSSTGYLTYYQAKSFALPGDWLVLEKPDVQL  
 FT TQCHMSIIVETNTPRDLRHGRVHVVEGNFRHASSRAPV  
 FT SREELMTVLSRLADVRIQGLYETETQRLTSLSEVGLREASDT  
 FT GSGRIALAVEICAPPAYAGDSC (in isoform B).  
 FT /FTID=VSP 003037.  
 FT W -> R (IN REF. 2).  
 FT CONFLICT 123 125  
 FT CONFLICT 481 481 ATG -> GAC (IN REF. 2).  
 FT CONFLICT 754 754 R -> K (IN REF. 2).  
 FT CONFLICT 969 969 E -> L (IN REF. 2).  
 FT CONFLICT 1052 1052 E -> Q (IN REF. 2).  
 FT CONFLICT 1184 1184 D -> A (IN REF. 2).  
 FT CONFLICT 1184 1184 G -> A (IN REF. 2).  
 SQ SEQUENCE 1713 AA; 189304 MW; 45EA9BE1017B60D3 CRC64;  
 Query Match 18.9%; Score 68.5; DB 1; Length 1713;  
 Best Local Similarity 36.1%; Pred.No.18;  
 Matches 22; Conservative 11; Mismatches 21; Indels 7; Gaps 3;  
 QY 9 VDGAAAAGCGQTSNDAAAEALN--ASSKEEALQ-IIREKIPKYLQFHHNLNSNLDRIFD 65  
 Db 553 VDAATAYENILNAIKAEADAANRAASASASALQTVIKEDLPK-----AKTLSSNSDKLLN 608  
 QY 66 K 66  
 Db 609 E 609  
 Search completed: December 23, 2003, 08:57:35  
 Job time : 7.77778 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: December 23, 2003, 08:51:23 ; Search time 25.3333 Seconds  
(without alignment)  
713.040 Million cell updates/sec

Title: US-09-289-346B-2  
Perfect score: 362  
Sequence: 1 TLVNGEFQVDCAAAGGQCT.....FQFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:\*\*

- 1: sp\_archaea:\*\*
- 2: sp\_bacteria:\*\*
- 3: sp\_fungi:\*\*
- 4: sp\_human:\*\*
- 5: sp\_invertebrate:\*\*
- 6: sp\_mammal:\*\*
- 7: sp\_mhc:\*\*
- 8: sp\_organelle:\*\*
- 9: sp\_page:\*\*
- 10: sp\_plant:\*\*
- 11: sp\_rodent:\*\*
- 12: sp\_virus:\*\*
- 13: sp\_vertibrate:\*\*
- 14: sp\_unclassified:\*\*
- 15: sp\_virus:\*\*
- 16: sp\_bacteriap:\*\*
- 17: sp\_archaeap:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	300	82.9	351	Q91R10	Q91R10 tomato seve
2	298	82.3	352	Q9E000	Q9E000 tomato rugo
3	290	80.1	232	Q8QPV3	Q8QPV3 tomato chlo
4	281	77.6	226	Q9WHF6	Q9WHF6 tomato mild
5	281	77.6	226	O09727	O09727 leonurus mo
6	279	77.1	361	Q67574	Q67574 bean golden
7	277	76.5	225	Q9QDB1	Q9QDB1 cowpea gold
8	277	76.5	314	Q9ELF8	Q9ELF8 sweet potat
9	277	76.5	364	Q9QSS5	Q9QSS5 sweet potat
10	274	75.7	185	Q98693	Q98693 sida golden
11	270	74.6	235	Q8QPU4	Q8QPU4 tomato infe
12	269	74.3	208	Q8JLY3	Q8JLY3 potato yell
13	269	74.3	289	Q8JLY5	Q8JLY5 potato yell
14	266	73.5	149	Q98975	Q98975 macroptiliu
15	266	73.5	233	Q9YLA4	Q9YLA4 macroptiliu
16	265	73.2	361	Q8JMJ4	Q8JMJ4 potato yell

17	263	72.7	360	12	Q8QMH4	Q8QMH4 sida mottle
18	261	72.1	361	12	Q8QVH0	Q8QVH0 ageratum en
19	260	71.8	234	12	O39180	O39180 geminivirid
20	258	71.3	223	12	Q8QPU7	Q8QPU7 tomato seve
21	257	71.0	190	12	Q9Z089	Q9Z089 tobacco lea
22	257	71.0	190	12	Q9Z084	Q9Z084 tobacco lea
23	256	70.7	190	12	Q9W827	Q9W827 tobacco lea
24	256	70.7	208	12	Q9Z0C4	Q9Z0C4 tobacco lea
25	256	70.7	359	12	Q91M88	Q91M88 tobacco lea
26	256	70.7	359	12	Q8JVE8	Q8JVE8 tomato curl
27	254	70.2	208	12	Q9Z0C0	Q9Z0C0 tobacco lea
28	254	70.2	208	12	Q9Z0B8	Q9Z0B8 tobacco lea
29	252	69.6	208	12	Q9Z0B6	Q9Z0B6 tobacco lea
30	251	69.3	203	12	Q9Z083	Q9Z083 tobacco lea
31	251	69.3	363	12	O73577	O73577 cotton leaf
32	246	68.0	359	12	Q91B86	Q91B86 ageratum ye
33	246	68.0	360	12	Q9DX10	Q9DX10 ageratum ye
34	244	67.4	208	12	Q9Z0A0	Q9Z0A0 tobacco lea
35	244	67.4	363	12	O72719	O72719 cotton leaf
36	244	67.4	363	12	O72705	O72705 cotton leaf
37	243	67.1	190	12	Q9Z086	Q9Z086 tobacco lea
38	243	67.1	208	12	Q9Z0C6	Q9Z0C6 tobacco lea
39	242	66.9	349	12	Q88888	Q88888 tomato pseu
40	242	66.9	362	12	O56816	O56816 chayote mos
41	241	66.6	359	12	Q9YZV4	Q9YZV4 tomato yell
42	241	66.6	359	12	Q9YUX7	Q9YUX7 tomato yell
43	241	66.6	359	12	Q9YL27	Q9YL27 tomato yell
44	241	66.6	359	12	Q9YZV2	Q9YZV2 tomato yell
45	241	66.6	364	12	Q8V5Z4	Q8V5Z4 ipomoea lea

ALIGNMENTS

RESULT 1

Q91R10 PRELIMINARY; PRT; 351 AA.  
ID Q91R10;  
AC Q91R10;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Rep protein.  
GN AC1.  
OS Tomato severe rugose virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=158463;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Minas Gerais;  
RA Rezende W.L., Goulart L.R., Parreira K.S., Figueiredo J.E.F.;  
RT "The full-length DNA-A nucleotide sequence of a novel tomato-infecting  
RL begomovirus, Tomato severe rugose virus, in Brazil.";  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY029750; AAKS0357.1; -  
DR InterPro; IPR001191; Geminini AL1.  
DR Pfam; PF00799; Geminini AL1; 1.  
DR PRINTS; PR00227; GEMCOATALL.  
DR Probdom; PD000736; Geminini AL1; 1.  
SQ SEQUENCE 351 AA; 40122 MW; 87F937A4F873B6CF CRC64;

Query Match 82.9%; Score 300; DB 12; Length 351;  
Best Local Similarity 78.6%; Pred. No. 1.3e-25;  
Matches 55; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLVNGEFQVDCAAAGGQCTSNDAALNASSKEALQIIREKIPEKYLQFHNLNSNL 60

Db 111 TIENGEGIDRSARGGCQTANDAAALNAPSXDVALQIIREKLPKFLQFHNLNSNL 170

QY 61 DRIFDKTPEP 70

Db 171 DRIFARAPEP 180

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Db      110 TLEWGEFQIDGRSARGGQQTNDAAAEALNASSKEAMQIIEKLPKFQYHNLSNL 169
Qy      61 DRIFDKTPEP 70
          ||||| |||
Db      170 DRIFSKAPEP 179

RESULT 4
Q9WHF6 PRELIMINARY; PRT; 226 AA.
ID AC Q9WHF6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Replication-associated protein (Fragment).
GN REP.
OS Tomato mild mottle geminivirus.
OC Viruses; ssDNA viruses; Geminiviridae; unclassified Geminiviridae.
NCBI_TaxID=92943;
[1]
RN RN SEQUENCE FROM N.A.
RC STRAIN=HN96-H5kw;
RA Nakha M.K., Mejia L., Ramirez P., Karkashian J.P., Doyle M.M., Maxwell D.P.;
RT "Molecular characterization and DNA-based detection methods for vegetable-infecting geminiviruses in Central America.";
RL Submitted (FEb-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AF131071; AAD33471.1; -
DR InterPro; IPR001191; Gemini_AL1.
PFam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
DR NON TER 226
SQ SEQUENCE 226 AA; 25941 MW; 2EA4116712871A23 CRC64;

Query Match 77.6%; Score 281; DB 12; Length 226;
Best Local Similarity 72.9%; Pred. No. 1.1e-23;
Matches 51; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy      1 TLVWGFEQVDGAAAAGGCOTSDNDAEALNASSKEARLQIREKIPEKFLQFHNLNSNL 60
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      111 TIWVGFEQIDGRSARGGQQTANDAAAEALNASSKEAMRIIEKLPKFQYHNLSNL 170
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      61 DRIFDKTPEP 70
          ||||| |||
Db      171 DRIFSKAPEP 180

RESULT 5
O09727 PRELIMINARY; PRT; 226 AA.
ID AC O09727;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE REP protein (Fragment).
GN REP.
OS Leovirus mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=58177;
[1]
RN RN SEQUENCE FROM N.A.
RC STRAIN=LmV- Brazil 1;
RA Faria J.C., Maxwell D.P.;
RT "Variability in geminivirus associated with Phaseolus vulgaris in Brazil.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
EMBL: U92533; AAB51157.1; --
DR InterPro; IPR001191; Gemini_AL1.
PFam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
DR NON TER 226
FT FT

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```

SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;
Query Match 77.6%; Score 281; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 1.1e-23;
Matches 54; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDCGAAAGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 60
Db 111 :|||||: :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
TVWGEFQVDCGRRSGGCGTNDAAAEALNAPDKRTALQIIREKIPEKYLFOFHNLSNLDRI 170

Qy 61 DRIFDKTPEP 70
Db 171 DRIFAKAPEP 180

RESULT 6
Q67574 PRELIMINARY; PRT; 361 AA.
AC Q67574;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative replicative protein.
GN ALI.
OS Bean Golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;

[1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RA "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration.";
RL Phytopathology 81:980-985(1991).
RN [2]

RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RA "Differentiation of bean-infecting geminiviruses by nucleic acid
RT hybridization probes and aspects of bean golden mosaic in Brazil.";
RL Plant Dis. 75:336-342(1991).
RN [3]

RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RA "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus.";
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M88686; AAA46312.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR PRODOM; PD000736; Geminini_AL1; 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 77.1%; Score 279; DB 12; Length 361;
Best Local Similarity 76.1%; Pred. No. 3.3e-23;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 4 WGEFQVDCGAAAGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63
Db 113 WGHFQVDCGRRSGGCGTNDAAAEALNASSKEEAMQIIREKIPEKYLFOFHNLSNLDRI 172

Qy 64 FDKTPEP 70
Db 173 FTKAPDP 179

RESULT 7
Q9QDB1 PRELIMINARY; PRT; 225 AA.
ID Q9QDB1
AC Q9QDB1;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Cowpea golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGMV-BR;
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RT Brazil.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF188708; AAF06318.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR PRODOM; PD000736; Geminini_AL1; 1.
FT NON TER 225 225
SQ SEQUENCE 225 AA; 25766 MW; 1089CB6BD8D15B5D CRC64;

Query Match 76.5%; Score 277; DB 12; Length 225;
Best Local Similarity 76.1%; Pred. No. 3.1e-23;
Matches 51; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 4 WGEFQVDCGAAAGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63
Db 113 WGHFQVDCGRRSGGCGTNDAAAEALNASSKEEAMQIIREKIPEKYLFOFHNLSNLDRI 172

Qy 64 FDKTPEP 70
Db 173 FKXPEP 179

RESULT 8
Q9ELT8 PRELIMINARY; PRT; 314 AA.
ID Q9ELT8
AC Q9ELT8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Replication association protein.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RA "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288227; AAG01006.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR PRODOM; PD000736; Geminini_AL1; 1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 76.5%; Score 277; DB 12; Length 314;
Best Local Similarity 79.4%; Pred. No. 4.6e-23;
Matches 54; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDCGAAAGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 60
Db 110 TITWGEFQVDCGRRSGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 169

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QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 9
Q9QS55 PRELIMINARY; PRT; 364 AA.
AC Q9QS55;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RT virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0 (1999).
DR EMBL; AF104036; RAD47173.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Geminini_AL1; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 76.58; Score 277; DB 12; Length 364;
Best Local Similarity 79.4%; Pred. No. 5.5e-23;
Matches 54; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGAAAGCGCOTSDAAAEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
Db 110 TIWGEFQIDGRSARGGQQTANDAAEALNASSKEALQIIREKIPKYLFOFHNLSNL 169
QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica;
RA Roy M.E., McLaughlin W.A., Nakhla N.K., Maxwell D.P.;
RT "Genetic Diversity among geminiviruses associated with the weed
RT species Sida spp. Macroptilium lathyroides, and Wissadula amplissima
RT from Jamaica.";
RL Plant Dis. 81:1251-1258 (1997).
DR EMBL; U67926; AAB97865.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.

QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 11
Q8QPU4 PRELIMINARY; PRT; 235 AA.
AC Q8QPU4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=MG-B11;
RA Ribeiro S.G., Ambrozovicus L.P., de Avila A.C., Calegario R.F.,
RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049208; AAL82833.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR ProDom; PD000736; Geminini_AL1; 1.
FT NON_TER 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BE0DD9C810 CRC64;

Query Match 74.6%; Score 270; DB 12; Length 235;
Best Local Similarity 73.1%; Pred. No. 2e-22;
Matches 49; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 4 WGEFQVDGAAAGCGCOTSDAAAEALNASSKEALQIIREKIPKYLFOFHNLSNLDRI 63
Db 113 WGIFQIDGRSARGGQQTANDAAEALNASSKEALQIIREKIPKYLFOFHNLSNLDRI 172
QY 64 DRIFDKTP 70
Db 173 FTKAPDP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

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RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126611; AAM95995.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALI.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 208
SQ SEQUENCE 208 AA; 23667 MW; 51211D58FAD690A6 CRC64;

Query Match 74.3%; Score 269; DB 12; Length 208;
Best Local Similarity 70.0%; Pred. No. 2.3e-22;
Matches 49; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
Db 110 TIEMGFQIDGRSARGGQTSNDAAAEALNSGAKEMKIIKEKLPKFLFOYHNLSSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 DRIFWKAPKP 179

RESULT 13
Q8JLY5 PRELIMINARY; PRT; 289 AA.
AC Q8JLY5;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;
RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126610; AAM95993.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALI.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 289
SQ SEQUENCE 289 AA; 32971 MW; 4ECF52F4C69C6764 CRC64;

Query Match 74.3%; Score 269; DB 12; Length 289;
Best Local Similarity 70.0%; Pred. No. 3.4e-22;
Matches 49; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
Db 110 TIEMGFQIDGRSARGGQTSNDAAAEALNSGAKEMKIIKEKLPKFLFOYHNLSSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 DRIFWKAPKP 179

RESULT 14
P88975 PRELIMINARY; PRT; 149 AA.
AC P88975;
DT 01-MAY-1997 (TremBLrel. 03, Created)
DT 01-MAY-1997 (TremBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;

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RN SEQUENCE FROM N.A.
RP STRAIN=Jamaican;
RA Roye M.E.;
RL Thesis (1996), Biochemistry, University of the West Indies, Jamaica.
DR EMBL; U75278; AAB36919.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALI.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 149
SQ SEQUENCE 149 AA; 16785 MW; E4CF5ED4C9CD508 CRC64;

Query Match 73.5%; Score 266; DB 12; Length 149;
Best Local Similarity 68.6%; Pred. No. 3.3e-22;
Matches 48; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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Db 52 TIEMGFQIDGRSARGGQTSNDAAAEALNSGAKEMKIIKEKLPKFLFOYHNLSSNL 111

Qy 61 DRIFDKTPEP 70
Db 112 DRIFWKDPEP 121

RESULT 15
Q9YLA4 PRELIMINARY; PRT; 233 AA.
AC Q9YLA4;
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
RN [1]
RP SEQUENCE FROM N.A.
RA Roye M.E.;
RT "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica strain 1;
RA Roye M.E., McLaughlin W.A., Maxwell D.P.;
RT "Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098940; AAD17850.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALI.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 233
SQ SEQUENCE 233 AA; 26356 MW; AA490AF4D2166A02 CRC64;

Query Match 73.5%; Score 266; DB 12; Length 233;
Best Local Similarity 68.6%; Pred. No. 5.7e-22;
Matches 48; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDGAAAGGCGTSDNDAAEALNASSKEALQIIREKIPKYLFOFHNLSNL 60
Db 110 TIEMGFQIDGRSARGGQTSNDAAAEALNSGAKEMKIIKEKLPKFLFOYHNLSSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 DRIFWKDPEP 179

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Search completed: December 23, 2003, 09:03:34  
Job time : 27.3333 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds  
(without alignments)  
340.128 Million cell updates/sec

Title: US-09-289-346B-3

Perfect score: 358

Sequence: 1 TLVNGEFQVDCRSARGGQGT.....QFENLNSNLDRIPTKPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	358	100.0	70	21	AA18679
2	347	96.9	70	21	AA18691
3	343	95.8	70	21	AA18690
4	332	92.7	70	21	AA18677
5	332	92.7	356	21	AA18687
6	324	90.5	70	21	AA18685
7	321	89.7	70	21	AA18688
8	320	89.4	70	21	AA18692
9	318	88.8	70	21	AA18684

10	317	88.5	70	21	AA18678
11	317	88.5	70	21	AA18686
12	316	88.3	70	21	AA18689
13	314	87.7	70	21	AA18680
14	311	86.9	70	21	AA18681
15	310	86.6	70	21	AA18683
16	308	86.0	70	21	AA18682
17	218	60.9	361	18	AAW34336
18	218	60.9	361	18	AAW34324
19	218	60.9	361	18	AAW34325
20	218	60.9	361	18	AAW34326
21	217	60.6	353	18	AAW34338
22	217	60.6	353	18	AAW34332
23	217	60.6	353	18	AAW34333
24	217	60.6	353	18	AAW34334
25	217	60.6	353	18	AAW34335
26	215	60.1	353	8	AAW70407
27	212	59.2	359	17	AAW88870
28	212	59.2	359	17	AAW88871
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30	200.5	56.0	361	8	AAW70562
31	198	55.3	362	19	AAW56495
32	191.5	53.5	50	23	AAO22043
33	190	53.1	357	18	AAW34337
34	190	53.1	357	18	AAW34329
35	190	53.1	357	18	AAW34330
36	190	53.1	357	18	AAW34331
37	85	23.7	142	24	ABP58120
38	73.5	20.5	270	23	ABW89877
39	73.5	20.5	304	22	AAW39860
40	73.5	20.5	406	22	AAW32868
41	73.5	20.5	425	22	AAW74314
42	73.5	20.5	427	22	AAW41646
43	69	19.3	577	19	ABW64982
44	66	18.4	508	22	ABW71345
45	65	18.2	548	22	ABW59192

#### ALIGNMENTS

#### RESULT 1

AA18679  
ID AA18679 standard; peptide; 70 AA.  
XX  
AC AA18679;  
XX  
22-JAN-2001 (first entry)  
XX  
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
XX  
Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
ribosome binding region; resistance; geminivirus infection.  
XX  
Synthetic.  
OS Tomato golden mosaic virus.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 27  
FT FT  
FT Misc-difference 30 /note= "wild type residue replaced with Ala"  
FT FT  
FT Misc-difference 34 /note= "wild type residue replaced with Ala"  
FT FT  
FT Misc-difference 35 /note= "wild type residue replaced with Ala"  
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FT Misc-difference 36 /note= "wild type residue replaced with Ala"  
XX  
WC200054573-A1.  
XX  
21-SEP-2000.  
XX

Mutant peptide der  
Mutant peptide der  
Mutant peptide der  
Mutant peptide der  
Mutant peptide der  
Mutant peptide der  
Tomato mottle viru  
Tomato mottle viru  
Tomato mottle viru  
Tomato mottle viru  
Bean golden mosaic  
Bean golden mosaic  
Bean golden mosaic  
Bean golden mosaic  
ORF 4 gene product  
Sardinian tomato Y  
Sardinian tomato Y  
Product of ORF 4 f  
Tobacco leaf curl  
Retinoblastoma-bin  
Tomato yellow leaf  
Tomato yellow leaf  
Tomato yellow leaf  
Tomato yellow leaf  
Human polypeptide  
Human polypeptide  
Human protein sequ  
Human splicing fac  
Human polypeptide  
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Drosophila melanog  
Drosophila melanog

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PF 15-MAR-2000; 2000WO-US06759.
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XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX PA
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
XX Claim 52; Page 43; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC plant imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 100.0%; Score 358; DB 21; Length 70;
XX Best Local Similarity 100.0%; Pred. No. 5.8e-39;
XX Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TLVWGEFQVDRSGRGCGCTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
DB 1 TLVWGEFQVDRSGRGCGCTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
XX
RESULT 2
AAB18691
ID AAB18691 standard; peptide; 70 AA.
XX AC
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 34 /note= "wild type residue replaced with Ala"
XX
XX Misc-difference 35 /note= "wild type residue replaced with Ala"
XX
XX Misc-difference 36 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.

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XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX PA
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
XX Disclosure; Page 49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC plant imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 96.9%; Score 347; DB 21; Length 70;
XX Best Local Similarity 97.1%; Pred. No. 1.6e-37;
XX Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 TLVWGEFQVDRSGRGCGCTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
DB 1 TLVWGEFQVDRSGRGCGCTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
XX
RESULT 3
AAB18690
ID AAB18690 standard; peptide; 70 AA.
XX AC
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 27 /note= "wild type residue replaced with Ala"
XX
XX Misc-difference 30 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.

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PN WO2000054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Disclosure; Page 49; 73pp; English.  
 XX The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX Sequence 70 AA;  
 SQ Query Match 95.8%; Score 343; DB 21; Length 70;  
 Best Local Similarity 95.7%; Pred. No. 5.3e-37;  
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIRKPKYLFQFHNLSNL 60  
 Db 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIRKPKYLFQFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 Db 61 DRIFDKTPEP 70  
 RESULT 4  
 AAB18677  
 ID AAB18677 standard; peptide; 70 AA.  
 XX AC AAB18677;  
 XX 22-JAN-2001 (first entry)  
 XX Peptide fragment from Rep protein of TGMV (amino acids 110-179).  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.  
 XX Tomato golden mosaic virus.  
 XX WO2000054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX

PR 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 PI WPI; 2000-618851/59.  
 DR Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Disclosure; Page 18; 73pp; English.  
 XX The present sequence is derived from a geminivirus replication (Rep)  
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,  
 CC catalyzes cleavage and ligation of single-stranded DNA, and interacts  
 CC with other viral and host proteins. Mutants of the AL1 protein are used  
 CC to produce transgenic plants. The mutation in AL1 is present in a  
 CC ribosome binding region, and expression of mutant AL1 protein imparts  
 CC increased resistance to geminivirus infection in the plant. Mutant AL1  
 CC proteins are useful for producing plants having increased resistance or  
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,  
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl  
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato  
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,  
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or  
 CC beet curly top virus.  
 XX Sequence 70 AA;  
 SQ Query Match 92.7%; Score 332; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 1.4e-35;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIRKPKYLFQFHNLSNL 60  
 Db 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIRKPKYLFQFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 Db 61 DRIFDKTPEP 70  
 RESULT 5  
 AAB18687  
 ID AAB18687 standard; peptide; 356 AA.  
 XX AC AAB18687;  
 XX 22-JAN-2001 (first entry)  
 XX Amino acid sequence of a geminivirus replication protein of TGMV.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.  
 XX Tomato golden mosaic virus.  
 XX OS  
 XX Key Location/Qualifiers  
 FT Misc-difference 354 /note= "unspecified amino acid"  
 FT WO2000054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 PR

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XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX DR Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT -
XX PS
XX PS Disclosure; Page 47-48; 73pp; English.
XX CC The present sequence represents a geminivirus replication (Rep)
XX CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
XX CC catalyzes cleavage and ligation of single-stranded DNA, and interacts
XX CC with other viral and host proteins. Mutants of the AL1 protein are used
XX CC to produce transgenic plants. The mutation in AL1 is present in a
XX CC ribosome binding region, and expression of mutant AL1 protein imparts
XX CC increased resistance to geminivirus infection in the plant. Mutant AL1
XX CC proteins are useful for producing plants having increased resistance or
XX CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
XX CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
XX CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
XX CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
XX CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
XX CC beet curly top virus.
XX SQ Sequence 356 AA;
XX Query Match 92.7%; Score 332; DB 21; Length 356;
XX Best Local Similarity 92.9%; Pred. No. 1.1e-34;
XX Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGFQVDRGARGCGCQTSNDAAAALAAASGAALQIIRKIPKYLQFPHNLNSNL 60
DB 110 TLVWGFQVDRGARGCGCQTSNDAAAALAAASGAALQIIRKIPKYLQFPHNLNSNL 169
QY 61 DRIFDKTPEP 70
DB 170 DRIFDKTPEP 179
XX RESULT 6
XX AAB18685
XX ID AAB18685 standard; peptide; 70 AA.
XX AC AAB18685;
XX DT 22-JAN-2001 (first entry)
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX PH Key Location/Qualifiers
XX FT Misc-difference 10 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 10 /note= "wild type residue replaced with Ala"
XX PN WO200054573-Al.
XX XX
XX PD 21-SEP-2000.
XX XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX XX

XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX DR Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT -
XX PS
XX PS Claim 53; Page 46; 73pp; English.
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
XX CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
XX CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
XX CC beet curly top virus.
XX SQ Sequence 70 AA;
XX Query Match 90.5%; Score 324; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 1.6e-34;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 TLVWGFQVDRGARGCGCQTSNDAAAALAAASGAALQIIRKIPKYLQFPHNLNSNL 60
DB 1 TLVWGFQVDRGARGCGCQTSNDAAAALAAASGAALQIIRKIPKYLQFPHNLNSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
XX RESULT 7
XX AAB18688
XX ID AAB18688 standard; peptide; 70 AA.
XX AC AAB18688;
XX DT 22-JAN-2001 (first entry)
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX PH Key Location/Qualifiers
XX FT Misc-difference 19 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 20 /note= "wild type residue replaced with Ala"
XX PN WO200054573-Al.
XX XX
XX PD 21-SEP-2000.
XX XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX XX

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XX (UUNC-) UNIV NORTH CAROLINA STATE.  
 XX PA Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX PI WPI; 2000-618851/59.  
 XX DR Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX PS Disclosure; Page 48; 73pp; English.  
 XX CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX SQ Sequence 70 AA;  
 Query Match 89.7%; Score 321; DB 21; Length 70;  
 Best Local Similarity 90.0%; Pred. No. 3.9e-34;  
 Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVGRSARGGCGTNDAAAALASSAAALQIREKIPEKYLQFHNLSNL 60  
 DB 1 TLVWGEFQVGRSARGGCGTNDAAAALASSAAALQIREKIPEKYLQFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 8  
 AAB18692  
 ID AAB18692 standard; peptide; 70 AA.  
 AC AAB18692;  
 DT 22-JAN-2001 (first entry)  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX Synthetic.  
 OS Tomato golden mosaic virus.  
 XX Key Location/Qualifiers  
 FH Misc-difference 66 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"  
 XX WO200054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.

PR 09-APR-1999; 99US-0289346.  
 XX (UUNC-) UNIV NORTH CAROLINA STATE.  
 XX PA Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX PI WPI; 2000-618851/59.  
 XX DR Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX PS Disclosure; Page 50; 73pp; English.  
 XX CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX SQ Sequence 70 AA;  
 Query Match 89.4%; Score 320; DB 21; Length 70;  
 Best Local Similarity 90.0%; Pred. No. 5.3e-34;  
 Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVGRSARGGCGTNDAAAALASSAAALQIREKIPEKYLQFHNLSNL 60  
 DB 1 TLVWGEFQVGRSARGGCGTNDAAAALASSAAALQIREKIPEKYLQFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 9  
 AAB18684  
 ID AAB18684 standard; peptide; 70 AA.  
 AC AAB18684;  
 DT 22-JAN-2001 (first entry)  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX Synthetic.  
 OS Tomato golden mosaic virus.  
 XX Key Location/Qualifiers  
 FH Misc-difference 7 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"  
 XX WO200054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.

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PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
PA (UYNC-) UNIV NORTH CAROLINA STATE.
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 52; Page 45; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 88.8%; Score 318; DB 21; Length 70;
XX Best Local Similarity 90.0%; Pred. No. 9.7e-34;
XX Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
Qy 1 TLVWGFQVDRSGCGCQTSNDAAAALAAASSAAALQIIRKIPKYLQFHNLSNL 60
Db 1 TLVWGEAVDGRSARGCGCQTSNDAAAALAAASSAAALQIIRKIPKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
XX
RESULT 10
AAB18678
ID AAB18678 standard; peptide; 70 AA.
XX
AC AAB18678;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 12 /note= "wild type residue replaced with Ala"
XX Misc-difference 13 /note= "wild type residue replaced with Ala"
XX Misc-difference 15 /note= "wild type residue replaced with Ala"
XX
XX WO2000054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 53; Page 42-43; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 88.8%; Score 317; DB 21; Length 70;
XX Best Local Similarity 88.8%; Pred. No. 1.3e-33;
XX Matches 62; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
XX
Qy 1 TLVWGFQVDRSGCGCQTSNDAAAALAAASSAAALQIIRKIPKYLQFHNLSNL 60
Db 1 TLVWGEAVDGRSARGCGCQTSNDAAAALAAASSAAALQIIRKIPKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
XX
RESULT 11
AAB18686
ID AAB18686 standard; peptide; 70 AA.
XX
AC AAB18686;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 24 /note= "wild type residue replaced with Leu"
XX Misc-difference 25 /note= "wild type residue replaced with Leu"
XX Misc-difference 26 /note= "wild type residue replaced with Leu"
XX
XX WO2000054573-A1.
XX
XX 21-SEP-2000.
XX

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PN WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX PA
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX
PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT -
XX
PS Claim 53; Page 46; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 88.5%; Score 317; DB 21; Length 70;
Best Local Similarity 88.6%; Pred. No. 1.3e-33;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIREKIPKYLFOFHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTSDNLLLEALNASSKEALQIREKIPKYLFOFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
XX
RESULT 12
AAB18689
ID AAB18689 standard; peptide; 70 AA.
XX
AC AAB18689;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
OS Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 22 /note= "wild type residue replaced with Ala"
FT Misc-difference 23 /note= "wild type residue replaced with Ala"
FT Misc-difference 23 /note= "wild type residue replaced with Ala"
FT Misc-difference 43

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XX WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX PA
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX
PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT -
XX
PS Disclosure; Page 48-49; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 88.3%; Score 316; DB 21; Length 70;
Best Local Similarity 90.0%; Pred. No. 1.8e-33;
Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIREKIPKYLFOFHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTSAALAAALNASSKEALQIREKIPKYLFOFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
XX
RESULT 13
AAB18680
ID AAB18680 standard; peptide; 70 AA.
XX
AC AAB18680;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
OS Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 42 /note= "wild type residue replaced with Ala"
FT Misc-difference 43

```

```

FT FT /note= "wild type residue replaced with Ala"
FT Misc-difference 44
FT FT /note= "wild type residue replaced with Ala"
XX XX
XX PN WO200054573-A1.
XX PD 21-SEP-2000.
XX XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX XX
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX XX
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX XX
XX FT Transgenic plants with increased resistance to geminivirus infection
XX FT comprise a nucleic acid construct containing a nucleic acid sequence
XX FT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX FT
XX PS Claim 52; Page 43-44; 73pp; English.
XX XX
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
XX
XX Query Match 87.7%; Score 314; DB 21; Length 70;
XX Best Local Similarity 88.6%; Pred. No. 3.2e-33;
XX Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 1 TLVWGEFQVDRSGRGCGCQTSDNDAALAAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
XX |||||||
XX DB 1 TLVWGEFQVDRSGRGCGCQTSDNDAALAAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
XX |||||||
XX QY 61 DRIFDKTPEP 70
XX |||||||
XX DB 61 DRIFDKTPEP 70
XX
XX RESULT 14
XX AAB18681
XX ID AAB18681 standard; peptide; 70 AA.
XX AC AAB18681;
XX XX
XX DT 22-JAN-2001 (first entry)
XX XX
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX XX
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX XX
XX FH Key Location/Qualifiers

```

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FT FT /note= "wild type residue replaced with Ala"
FT Misc-difference 48
FT FT /note= "wild type residue replaced with Ala"
XX XX
XX FT Misc-difference 49
XX FT /note= "wild type residue replaced with Ala"
XX PN WO200054573-A1.
XX XX
XX PD 21-SEP-2000.
XX XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX XX
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX XX
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX XX
XX DR WPI; 2000-618851/59.
XX XX
XX FT Transgenic plants with increased resistance to geminivirus infection
XX FT comprise a nucleic acid construct containing a nucleic acid sequence
XX FT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX FT
XX PS Claim 52; Page 44; 73pp; English.
XX XX
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
XX
XX Query Match 86.9%; Score 311; DB 21; Length 70;
XX Best Local Similarity 88.6%; Pred. No. 8e-33;
XX Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 1 TLVWGEFQVDRSGRGCGCQTSDNDAALAAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
XX |||||||
XX DB 1 TLVWGEFQVDRSGRGCGCQTSDNDAALAAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
XX |||||||
XX QY 61 DRIFDKTPEP 70
XX |||||||
XX DB 61 DRIFDKTPEP 70
XX
XX RESULT 15
XX AAB18683
XX ID AAB18683 standard; peptide; 70 AA.
XX AC AAB18683;
XX XX
XX DT 22-JAN-2001 (first entry)
XX XX
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX XX
XX OS Synthetic.

```





```
Db 110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNRSL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 2
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match 60.9%; Score 218; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 4.le-21;
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLWGFQVDGRSARGGQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 60
Db 110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNRSL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 3
US-08-838-151A-6
; Sequence 6, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6

Query Match 60.9%; Score 218; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 4.le-21;
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLWGFQVDGRSARGGQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 60
Db 110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNRSL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179
```

```
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6

Query Match 60.9%; Score 218; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 4.le-21;
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLWGFQVDGRSARGGQTSNDAAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 60
Db 110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNRSL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 4
US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
```

```
; MOLECULE TYPE: protein
; US-08-838-151A-46

Query Match      60.6%; Score 217; DB 3; Length 353;
Best Local Similarity 58.6%; Pred.No. 5.4e-21;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY   1 TLWGFEFQVDRSGRGCGCOTSDNDAAAALAAASAAAAAQIIRKIPKYLFQPHNLSNL 60
Db    110 TIEWGQFOVDGRSARGGQQSQANDSYAKALNADSIESTALTILKEEQPKDYVLQHINIRS NL 169
       :|::|||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY   61 DRIFDKTPEP 70
Db    170 ERIFVKVPEP 179
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 6
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

Query Match      60.6%; Score 217; DB 3; Length 353;
Best Local Similarity 58.6%; Pred.No. 5.4e-21;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY   1 TLWGFEFQVDRSGRGCGCOTSDNDAAAALAAASAAAAAQIIRKIPKYLFQPHNLSNL 60
Db    110 TIEWGQFOVDGRSARGGQQSQANDSYAKALNADSIESTALTILKEEQPKDYVLQHINIRS NL 169
       :|::|||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY   61 DRIFDKTPEP 70
Db    170 ERIFVKVPEP 179
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```



```
RESULT 7
US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-49
Query Match 60.6%; Score 217; DB 3; Length 353;
Best Local Similarity 58.6%; Pred. No. 5.4e-21;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
Qy 1 TLVWGEFQVDSRGSGGQTSNDAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
Db 110 TIEWGQFQVDSRGSGGQTSNDAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179
;
RESULT 8
US-08-838-151A-52
; Sequence 52, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
```

```
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-52
Query Match 60.6%; Score 217; DB 3; Length 353;
Best Local Similarity 58.6%; Pred. No. 5.4e-21;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
Qy 1 TLVWGEFQVDSRGSGGQTSNDAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
Db 110 TIEWGQFQVDSRGSGGQTSNDAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179
;
RESULT 9
US-08-838-151A-55
; Sequence 55, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
```



```
US-08-809-103B-6
; Sequence 6, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-6

Query Match          59.2%; Score 212; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 2.6e-20;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY      2 LVWGEFQVDRGARGCGQTSNDAAAALAAASAAALQIIRKIKPEKYLQFPHNLSNLD 61
Db      111 LEWGTFTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVYLHFNHNSNLD 170

QY      62 RIFDKTPEP 70
Db      171 KVFQVPPAP 179

RESULT 13
US-08-809-103B-8
; Sequence 8, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
```

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; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8

Query Match          59.2%; Score 212; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 2.6e-20;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY      2 LVWGEFQVDRGARGCGQTSNDAAAALAAASAAALQIIRKIKPEKYLQFPHNLSNLD 61
Db      111 LEWGTFTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVYLHFNHNSNLD 170

QY      62 RIFDKTPEP 70
Db      171 KVFQVPPAP 179

RESULT 14
US-08-838-151A-20
; Sequence 20, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
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/
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mueller, Lisa V
/ REGISTRATION NUMBER: 38,978
/ REFERENCE/DOCKET NUMBER: SVS3801P0260
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-616-5400
/ TELEFAX: 312-616-5460
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 357 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-838-151A-20

Query Match 53.1%; Score 190; DB 3; Length 357;
Best Local Similarity 60.7%; Pred. No. 2.4e-17;
Matches 37; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 4 WGEFQVDGRSARGGCOTSDNDAALAAASAAAALQIIREKIPEKYLQFPHNLNSNLDRI 63
Db 111 FGVSIQDGRSARGGQSANDAYAEALNSGSISEALNLIKKEKPKDYILQFPHNLSSNLDRI 170

QY 64 F 64
Db 171 F 171

RESULT 15
US-08-838-151A-24
/ Sequence 24, Application US/08838151A
/ Patent No. 6291743
/ GENERAL INFORMATION:
/ APPLICANT: Stout, John T
/ APPLICANT: Luu, Hang T
/ APPLICANT: Maxwell, Douglas
/ APPLICANT: Ahlquist, Paul
/ APPLICANT: Hanson, Steve
/ TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
/ TITLE OF INVENTION: Genes
/ NUMBER OF SEQUENCES: 63
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dressler, Rockey, Milnamow & Katz
/ STREET: Two Prudential Plaza, Suite 4700
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: U.S.A.
/ ZIP: 60601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/838,151A
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mueller, Lisa V
/ REGISTRATION NUMBER: 38,978
/ REFERENCE/DOCKET NUMBER: SVS3801P0260
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-616-5400
/ TELEFAX: 312-616-5460
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 357 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-838-151A-24
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Query Match 53.1%; Score 190; DB 3; Length 357;
Best Local Similarity 60.7%; Pred. No. 2.4e-17;
Matches 37; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 4 WGEFQVDGRSARGGCOTSDNDAALAAASAAAALQIIREKIPEKYLQFPHNLNSNLDRI 63
Db 111 FGVSIQDGRSARGGQSANDAYAEALNSGSISEALNLIKKEKPKDYILQFPHNLSSNLDRI 170

QY 64 F 64
Db 171 F 171
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Search completed: December 23, 2003, 08:59:33  
Job time : 12.6667 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	358	100.0	70	10	US-09-289-346A-3	Sequence 3, Appl
2	347	96.9	70	10	US-09-289-346A-15	Sequence 15, Appl
3	343	95.8	70	10	US-09-289-346A-14	Sequence 14, Appl
4	332	92.7	70	10	US-09-289-346A-1	Sequence 1, Appl
5	332	92.7	356	10	US-09-289-346A-11	Sequence 11, Appl
6	324	90.5	70	10	US-09-289-346A-9	Sequence 9, Appl
7	321	89.7	70	10	US-09-289-346A-12	Sequence 12, Appl
8	320	89.4	70	10	US-09-289-346A-16	Sequence 16, Appl
9	318	88.8	70	10	US-09-289-346A-8	Sequence 8, Appl
10	317	88.5	70	10	US-09-289-346A-2	Sequence 2, Appl
11	317	88.5	70	10	US-09-289-346A-10	Sequence 10, Appl
12	316	88.3	70	10	US-09-289-346A-13	Sequence 13, Appl
13	314	87.7	70	10	US-09-289-346A-4	Sequence 4, Appl
14	311	86.9	70	10	US-09-289-346A-5	Sequence 5, Appl
15	310	86.6	70	10	US-09-289-346A-7	Sequence 7, Appl

QY 61 DRIFDKTPEP 70

61 DRIFDKTPEP 70

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Db 61 DRIFDKTPEP 70
|||||
RESULT 2
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match 96.9%; Score 347; DB 10; Length 70;
Best Local Similarity 97.1%; Pred. No. 2.4e-37;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDCRSARGGCGTSDNAAAALAAASSAAAALQIIREKIPEKYLQFHNLSNL 60
DB 1 TLVWGEFQVDCRSARGGCGTSDNAAAALAAASSAAAALQIIREKIPEKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70
|||||
Db 61 DRIFDKTPEP 70

RESULT 3
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14

Query Match 95.8%; Score 343; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 7.8e-37;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDCRSARGGCGTSDNAAAALAAASSAAAALQIIREKIPEKYLQFHNLSNL 60
DB 1 TLVWGEFQVDCRSARGGCGTSDNAAAALAAASSAAAALQIIREKIPEKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70
|||||
Db 61 DRIFDKTPEP 70

RESULT 4
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11

Query Match 92.7%; Score 332; DB 10; Length 356;
Best Local Similarity 92.9%; Pred. No. 1.6e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDCRSARGGCGTSDNAAAALAAASSAAAALQIIREKIPEKYLQFHNLSNL 60
DB 110 TLVWGEFQVDCRSARGGCGTSDNAAAALAAASSAAAALQIIREKIPEKYLQFHNLSNL 169

QY 61 DRIFDKTPEP 70
|||||
Db 61 DRIFDKTPEP 70

RESULT 5
US-9-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11

Query Match 92.7%; Score 332; DB 10; Length 356;
Best Local Similarity 92.9%; Pred. No. 1.6e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDCRSARGGCGTSDNAAAALAAASSAAAALQIIREKIPEKYLQFHNLSNL 60
DB 110 TLVWGEFQVDCRSARGGCGTSDNAAAALAAASSAAAALQIIREKIPEKYLQFHNLSNL 169
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QY      61 DRIFDKTPEP 70
Db      170 DRIFDKTPEP 179

RESULT 6
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRP
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9

Query Match      90.5%; Score 324; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 2.2e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 TLVWGFQVDGRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
Db      1 TLVWGFQVAGRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60

RESULT 7
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRP
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12

Query Match      89.7%; Score 321; DB 10; Length 70;
Best Local Similarity 90.0%; Pred. No. 5.5e-34;

QY      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

RESULT 8
US-09-289-346A-16
; Sequence 16, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 70
; TYPE: PRP
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-16

Query Match      89.4%; Score 320; DB 10; Length 70;
Best Local Similarity 90.0%; Pred. No. 7.4e-34;
Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 TLVWGFQVDGRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60
Db      1 TLVWGFQVDGRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60

RESULT 9
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRP
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)..(8)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
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; OTHER INFORMATION: replacements (TQ118->AA118).
; US-09-289-346A-8
Query Match      88.8%; Score 318; DB 10; Length 70;
Best Local Similarity 90.0%; Pred. No. 1.3e-33;
Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
DB 1 TLVWGEAAVDGSRARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-2
; Sequence 2, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
; OTHER INFORMATION: replacements (TQ118->AA118).
; US-09-289-346A-2
Query Match      88.5%; Score 317; DB 10; Length 70;
Best Local Similarity 88.6%; Pred. No. 1.8e-33;
Matches 62; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAA136->LLL136).
; OTHER INFORMATION: replacements (TQ118->AA118).
; US-09-289-346A-10
Query Match      88.5%; Score 317; DB 10; Length 70;
Best Local Similarity 88.6%; Pred. No. 1.8e-33;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAA136->LLL136).
; OTHER INFORMATION: replacements (TQ118->AA118).
; US-09-289-346A-13
Query Match      88.3%; Score 316; DB 10; Length 70;
Best Local Similarity 90.0%; Pred. No. 2.4e-33;
Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-4
; Sequence 4, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAA136->LLL136).
; OTHER INFORMATION: replacements (TQ118->AA118).
; US-09-289-346A-4
Query Match      88.8%; Score 318; DB 10; Length 70;
Best Local Similarity 90.0%; Pred. No. 1.3e-33;
Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
DB 1 TLVWGEAAVDGSRARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 14
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
; OTHER INFORMATION: replacements (TQ118->AA118).
; US-09-289-346A-8
Query Match      88.8%; Score 318; DB 10; Length 70;
Best Local Similarity 90.0%; Pred. No. 1.3e-33;
Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
DB 1 TLVWGEAAVDGSRARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 15
US-09-289-346A-2
; Sequence 2, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
; OTHER INFORMATION: replacements (TQ118->AA118).
; US-09-289-346A-2
Query Match      88.5%; Score 317; DB 10; Length 70;
Best Local Similarity 88.6%; Pred. No. 1.8e-33;
Matches 62; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTSDNDAALAAASSAAALQIIREKIPEKYLQFPHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 16
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAA136->LLL136).
; OTHER INFORMATION: replacements (TQ118->AA118).
; US-09-289-346A-10
Query Match      88.5%; Score
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; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; NAME/KEY: VARIANT
; LOCATION: (42)..(44)
; OTHER INFORMATION: Description of Artificial sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REK154->AAA154).
US-09-289-346A-4

Query Match      87.7%; Score 314; DB 10; Length 70;
Best Local Similarity 88.6%; Pred. No. 4.4e-33;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 1 TLVWGEFQVDRSGCGCQTSNDAAAALAAASSAAAAALQIIREKIPKYLQFHNLSNL 60

QY 61 DRIPDKTPEP 70
Db 61 DRIPDKTPEP 70

RESULT 14
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (SKY159->AAA159).
US-09-289-346A-5

Query Match      86.9%; Score 311; DB 10; Length 70;
Best Local Similarity 88.6%; Pred. No. 1.1e-32;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 1 TLVWGEFQVDRSGCGCQTSNDAAAALAAASSAAAAALQIIREKIPKYLQFHNLSNL 60

QY 61 DRIPDKTPEP 70
Db 61 DRIPDKTPEP 70
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RESULT 15
US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; NAME/KEY: VARIANT
; LOCATION: (59)..(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDR172->ALAA172).
US-09-289-346A-7

Query Match      86.6%; Score 310; DB 10; Length 70;
Best Local Similarity 88.6%; Pred. No. 1.1e-32;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGCGCQTSNDAAAALAAASSAAAAALQIIREKIPKYLQFHNLSNL 60
Db 1 TLVWGEFQVDRSGCGCQTSNDAAAALAAASSAAAAALQIIREKIPKYLQFHNLSNL 60

QY 61 DRIPDKTPEP 70
Db 61 DRIPDKTPEP 70

Search completed: December 23, 2003, 09:43:29
Job time : 77 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:56:38 ; Search time 163.778 Seconds  
(without alignments)  
388.907 Million cell updates/sec

Title: US-09-289-346B-3

Perfect score: 358

Sequence: 1 TLVWGEFQVDSRSGCQT.....FQPHNLNLDRIFDKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2\_6/ptodata/1/paa/US06 COMB.pcp.\*  
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4: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*  
5: /cgn2\_6/ptodata/1/paa/US081 COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/paa/US082 COMB.pcp.\*  
7: /cgn2\_6/ptodata/1/paa/US083 COMB.pcp.\*  
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27: /cgn2\_6/ptodata/1/paa/US101 COMB.pcp.\*  
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29: /cgn2\_6/ptodata/1/paa/US103 COMB.pcp.\*  
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32: /cgn2\_6/ptodata/1/paa/US60 COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	358	100.0	70	16	US-09-289-346A-3

Sequence 3, Appli

2	358	100.0	70	31	US-10-633-850-4
3	358	100.0	352	31	US-10-633-850-78
4	347	96.9	70	16	US-09-289-346A-15
5	347	96.9	70	31	US-10-633-850-15
6	347	96.9	352	31	US-10-633-850-64
7	343	95.8	70	16	US-09-289-346A-14
8	343	95.8	70	31	US-10-633-850-14
9	343	95.8	352	31	US-10-633-850-62
10	342	95.5	70	31	US-10-633-850-20
11	342	95.5	352	31	US-10-633-850-86
12	337	94.1	70	31	US-10-633-850-17
13	337	94.1	70	31	US-10-633-850-18
14	337	94.1	70	31	US-10-633-850-19
15	337	94.1	352	31	US-10-633-850-80
16	337	94.1	352	31	US-10-633-850-82
17	337	94.1	352	31	US-10-633-850-84
18	332	92.7	70	16	US-09-289-346A-1
19	332	92.7	70	31	US-10-633-850-2
20	332	92.7	352	31	US-10-633-850-1
21	332	92.7	356	16	US-09-289-346A-11
22	329	91.9	70	31	US-10-633-850-23
23	329	91.9	352	31	US-10-633-850-92
24	329	91.9	352	31	US-10-633-850-94
25	327	91.3	70	31	US-10-633-850-22
26	327	91.3	352	31	US-10-633-850-90
27	326	91.1	70	31	US-10-633-850-21
28	326	91.1	352	31	US-10-633-850-88
29	324	90.5	70	16	US-09-289-346A-9
30	324	90.5	70	31	US-10-633-850-10
31	324	90.5	70	31	US-10-633-850-24
32	324	90.5	352	31	US-10-633-850-96
33	322	89.9	70	31	US-10-633-850-25
34	322	89.9	352	31	US-10-633-850-98
35	321	89.7	70	16	US-09-289-346A-12
36	321	89.7	70	31	US-10-633-850-12
37	321	89.7	352	31	US-10-633-850-58
38	320	89.4	70	16	US-09-289-346A-16
39	320	89.4	70	31	US-10-633-850-16
40	320	89.4	352	31	US-10-633-850-74
41	318	88.8	70	16	US-09-289-346A-8
42	318	88.8	70	31	US-10-633-850-9
43	318	88.8	352	31	US-10-633-850-52
44	317	88.5	70	16	US-09-289-346A-2
45	317	88.5	70	16	US-09-289-346A-10

#### ALIGNMENTS

RESULT 1  
US-09-289-346A-3  
; Sequence 3, Application US/09289346A  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (27)..(36)  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of

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; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (EALNASSKEE->AALAASSAAA)
US-09-289-346A-3

Query Match      100.0%; Score 358; DB 16; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.5e-38;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCQTSDNDAALAAASSAAAAAQIIREKIPEKYLQFPHNLSNL 60
   |||||||
Db 1 TLVWGEFQVDRSARGCGCQTSDNDAALAAASSAAAAAQIIREKIPEKYLQFPHNLSNL 60
   |||||||

QY 61 DRIFDKTPEP 70
   |||||||
Db 61 DRIFDKTPEP 70
   |||||||

RESULT 2
US-10-633-850-4
; Sequence 4, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.458IP
; CURRENT APPLICATION NUMBER: US/10/633,850
; PRIOR FILING DATE: 2003-08-04
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: MICS_FEATURE
; LOCATION: (27)..(36)
; OTHER INFORMATION: E-N140 + KEE146 (Ala4+5) mutation
US-10-633-850-4

Query Match      100.0%; Score 358; DB 31; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.5e-38;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCQTSDNDAALAAASSAAAAAQIIREKIPEKYLQFPHNLSNL 60
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Db 1 TLVWGEFQVDRSARGCGCQTSDNDAALAAASSAAAAAQIIREKIPEKYLQFPHNLSNL 60
   |||||||

QY 61 DRIFDKTPEP 70
   |||||||
Db 61 DRIFDKTPEP 70
   |||||||

RESULT 3
US-10-633-850-78
; Sequence 78, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.458IP
; CURRENT APPLICATION NUMBER: US/10/633,850
; PRIOR FILING DATE: 2003-08-04
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: MICS_FEATURE
; LOCATION: (27)..(36)
; OTHER INFORMATION: E-N140 + KEE146 (Ala4+5) mutation
US-10-633-850-78

Query Match      96.9%; Score 347; DB 16; Length 70;
Best Local Similarity 97.1%; Pred. No. 4.2e-37;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 TLVWGEFQVDRSARGCGCQTSDNDAALAAASSAAAAAQIIREKIPEKYLQFPHNLSNL 60
   |||||||

QY 61 DRIFDKTPEP 70
   |||||||
Db 61 DRIFDKTPEP 70
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RESULT 4
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match      96.9%; Score 347; DB 16; Length 70;
Best Local Similarity 97.1%; Pred. No. 4.2e-37;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCQTSDNDAALAAASSAAAAAQIIREKIPEKYLQFPHNLSNL 60
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Db 1 TLVWGEFQVDRSARGCGCQTSDNDAALAAASSAAAAAQIIREKIPEKYLQFPHNLSNL 60
   |||||||

QY 61 DRIFDKTPEP 70
   |||||||
Db 61 DRIFDKTPEP 70
   |||||||

RESULT 5
US-10-633-850-15
; Sequence 15, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.458IP
; CURRENT APPLICATION NUMBER: US/10/633,850
; PRIOR FILING DATE: 2003-08-04
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-10-633-850-15

Query Match      100.0%; Score 358; DB 16; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.5e-38;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCQTSDNDAALAAASSAAAAAQIIREKIPEKYLQFPHNLSNL 60
   |||||||
Db 1 TLVWGEFQVDRSARGCGCQTSDNDAALAAASSAAAAAQIIREKIPEKYLQFPHNLSNL 60
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QY 61 DRIFDKTPEP 70
   |||||||
Db 61 DRIFDKTPEP 70
   |||||||
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; LENGTH: 70
; TYPE: PRF
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (34)..(36)
; OTHER INFORMATION: KEE146 (Ala5) mutation
US-10-633-850-15

Query Match      96.9%; Score 347; DB 31; Length 70;
Best Local Similarity 97.1%; Pred. No. 4.2e-37;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSARGGCQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGFQVDRSARGGCQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 6
US-10-633-850-64
; Sequence 64, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 352
; TYPE: PRF
; ORGANISM: Tomato golden mosaic virus
US-10-633-850-64

Query Match      96.9%; Score 347; DB 31; Length 352;
Best Local Similarity 97.1%; Pred. No. 3.4e-36;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSARGGCQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Db 111 TLVWGFQVDRSARGGCQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 170
Qy 61 DRIFDKTPEP 70
Db 171 DRIFDKTPEP 180

RESULT 7
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRF
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14

Query Match      95.8%; Score 343; DB 16; Length 70;
Best Local Similarity 95.7%; Pred. No. 1.4e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSARGGCQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGFQVDRSARGGCQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 8
US-10-633-850-14
; Sequence 14, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRF
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (27)..(30)
; OTHER INFORMATION: E--N140 (Ala4) mutation
US-10-633-850-14

Query Match      95.8%; Score 343; DB 31; Length 70;
Best Local Similarity 95.7%; Pred. No. 1.4e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSARGGCQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGFQVDRSARGGCQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 9
US-10-633-850-62
; Sequence 62, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
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; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-10-633-850-62

Query Match          95.8%; Score 343; DB 31; Length 352;
Best Local Similarity 95.7%; Pred. No. 1.1e-35;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60
Db 111 TLVWGEFQVDSARGGCGTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 170
QY 61 DRIFDKTPEP 70
Db 171 DRIFDKTPEP 180

RESULT 10
US-10-633-850-20
; Sequence 20, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; NAME/KEY: MISC FEATURE
; LOCATION: (35)..(36)
; OTHER INFORMATION: EE146 mutation
US-10-633-850-20

Query Match          95.5%; Score 342; DB 31; Length 70;
Best Local Similarity 95.7%; Pred. No. 1.9e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGEFQVDSARGGCGTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 11
US-10-633-850-86
; Sequence 86, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
```

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; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-10-633-850-86

Query Match          95.5%; Score 342; DB 31; Length 352;
Best Local Similarity 95.7%; Pred. No. 1.5e-35;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60
Db 111 TLVWGEFQVDSARGGCGTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 170
QY 61 DRIFDKTPEP 70
Db 171 DRIFDKTPEP 180

RESULT 12
US-10-633-850-17
; Sequence 17, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; NAME/KEY: MISC FEATURE
; LOCATION: (34)..(34)
; OTHER INFORMATION: K144 mutation
US-10-633-850-17

Query Match          94.1%; Score 337; DB 31; Length 70;
Best Local Similarity 94.3%; Pred. No. 8.6e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60
Db 1 TLVWGEFQVDSARGGCGTSDNDAALAAASAAAALQIIREKIPEKYLFOFHNLSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 13
US-10-633-850-18
; Sequence 18, Application US/10633850
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruissem, Wilhelm
```

; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: 5051.458IP  
; CURRENT APPLICATION NUMBER: US/10/633,850  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 09/289,346  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (35)..(35)  
; OTHER INFORMATION: E145 mutation  
US-10-633-850-18

Query Match 94.1%; Score 337; DB 31; Length 70;  
Best Local Similarity 94.3%; Pred. No. 8.6e-36;  
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 TLVWGEFQVDRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60  
Db 1 TLVWGEFQVDRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60  
Qy 61 DRIFDKTPEP 70  
Db 61 DRIFDKTPEP 70

RESULT 14  
US-10-633-850-19  
; Sequence 19, Application US/10633850  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: 5051.458IP  
; CURRENT APPLICATION NUMBER: US/10/633,850  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 09/289,346  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (36)..(36)  
; OTHER INFORMATION: E146 mutation  
US-10-633-850-19

Query Match 94.1%; Score 337; DB 31; Length 70;  
Best Local Similarity 94.3%; Pred. No. 8.6e-36;  
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 TLVWGEFQVDRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60  
Db 1 TLVWGEFQVDRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60  
Qy 61 DRIFDKTPEP 70  
Db 61 DRIFDKTPEP 70

RESULT 15  
US-10-633-850-80  
; Sequence 80, Application US/10633850  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: 5051.458IP  
; CURRENT APPLICATION NUMBER: US/10/633,850  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 09/289,346  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 80  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
US-10-633-850-80

Query Match 94.1%; Score 337; DB 31; Length 352;  
Best Local Similarity 94.3%; Pred. No. 7e-35;  
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 TLVWGEFQVDRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60  
Db 111 TLVWGEFQVDRSARGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLQFHNLSNL 170  
Qy 61 DRIFDKTPEP 70  
Db 171 DRIFDKTPEP 180

Search completed: December 23, 2003, 09:30:02  
Job time : 163.778 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds  
(without alignments)  
673.181 Million cell updates/sec

Title: US-09-289-346B-3  
Perfect score: 358  
Sequence: 1 TLVWGEFQVDSARGGCQT.....FQPHNLNSLDRIFDKTPEP 70

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:.\*  
1: Piri:.\*  
2: Piri:.\*  
3: Piri:.\*  
4: Piri:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	332	92.7	352	1 QOCVLI	AlI protein - toma
2	243	67.9	361	1 QOCVPT	AlI protein - toma
3	230	64.2	358	2 S07594	hypothetical prote
4	222	62.0	362	1 JQ1887	AlI protein - toma
5	217	60.6	355	1 QOCVM1	AVI protein - abut
6	216	60.3	349	2 JQ2300	replicase - pepper
7	216	60.3	349	2 S31875	AlI protein - pepp
8	216	60.3	359	2 S39211	gene C1 protein -
9	214	59.8	358	1 JQ1870	AlI protein - toma
10	213	59.5	351	2 JQ2327	AlI protein - Indi
11	212	59.2	359	2 S22593	hypothetical prote
12	208	58.1	360	2 S28360	AlI protein - beet
13	207	57.8	360	2 S59885	replication-associ
14	203	56.7	359	2 S39235	gene C1 protein -
15	190	53.1	357	1 QOCVC1	AlI protein - toma
16	120	33.5	131	2 S45059	AC1 protein (clone
17	115	32.1	347	1 QOCVSI	AlI protein - squa
18	69	19.3	577	2 S30237	transcription init
19	66	18.4	508	2 S59870	fork head domain p
20	65	18.2	840	2 T36375	probable large ATP
21	65	18.2	254	2 F97486	DNA repair protein
22	65	18.2	254	2 F97486	reco-like protein
23	65	18.2	671	2 A35912	homeotic protein o
24	63	17.6	392	2 T44362	acetyl-CoA C-acety
25	62.5	17.5	700	2 T05841	apliceosome-associ
26	62.5	17.5	1077	2 A44067	serine-rich protei
27	62	17.3	409	2 T16781	hypothetical prote
28	61.5	17.2	317	2 D89961	conserved hypothet
29	61.5	17.2	327	2 P83408	hypothetical prote

30 61.5 17.2 705 2 T31157  
31 61.5 17.2 1541 2 T02831  
32 61 17.0 339 2 T26328  
33 61 17.0 371 2 B69502  
34 61 17.0 1265 2 T47626  
35 61 17.0 1510 2 T33100  
36 60.5 16.9 509 2 T02942  
37 60.5 16.9 829 2 A34692  
38 60.5 16.9 883 2 S04722  
39 60 16.8 314 2 JCS273  
40 59.5 16.6 201 2 A81380  
41 59.5 16.6 244 2 B86197  
42 59.5 16.6 470 2 T46814  
43 59.5 16.6 470 2 B95419  
44 59.5 16.6 481 2 A70091  
45 59.5 16.6 509 2 T02940

hypothetical prote  
AAA protein I4171.  
hypothetical prote  
alcohol dehydrogen  
structural mainten  
hypothetical prote  
O-succinylhomoseri  
ecdysone-induced p  
puff 74E protein -  
paired type homeob  
probable flagellar  
hypothetical prote  
gamma-aminobutyrat  
diaminobutyrate-py  
probable phosphoes  
O-succinylhomoseri

ALIGNMENTS

RESULT 1

QOCVLI  
AlI protein - tomato golden mosaic virus  
C:Species: tomato golden mosaic virus  
A:Note: host Nicotiana sp. (tobacco)  
C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Apr-1994  
C:Accession: A04170  
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.  
EMBO J. 3, 2197-2205, 1984  
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat.  
A:Reference number: A04163  
A:Accession: A04170  
A:Molecule type: DNA  
A:Residues: 1-352 <HAM>  
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus AlI protein

Query Match 92.7%; Score 332; DB 1; Length 352;  
Best Local Similarity 92.9%; Pred. No. 4.8e-31;  
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 TLVWGEFQVDSARGGCQTSNDAAAALAAASAAAALQIIRKIPKYLQFPHNLNSL 60  
Db 111 TLVWGEFQVDSARGGCQTSNDAAAALAAASAAAALQIIRKIPKYLQFPHNLNSL 170  
Qy 61 DRIFDKTPEP 70  
Db 171 DRIFDKTPEP 180

RESULT 2

QOCVPT  
AlI protein - potato yellow mosaic virus (isolate Venezuela)  
C:Species: potato yellow mosaic virus  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jun-2000  
C:Accession: JU0364  
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.  
J. Gen. Virol. 72, 1515-1520, 1991  
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel.  
A:Reference number: JU0362; MUID:91311403; PMID:1856690  
A:Accession: JU0364  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-361 <COU>  
A:Cross-references: GB:D00940; NID:G222458; PIDN:BAA00782.1; PID:G222459  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus AlI protein

```
Query Match      67.9%; Score 243; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 1.2e-20;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
DB 110 TLEWGFQIDGRSARGGQQTVDNAAALNSGTKEAMKIIKEKLPKFLFOYHNLSNL 169

QY 61 DRIEDKTPPE 69
DB 170 DRIFWKAPE 178

RESULT 3
S07594
hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)
C:Species: cassava latent virus
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C:Accession: S07594
R:Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
Nucleic Acids Res. 18, 197-198, 1990
A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A:Reference number: S07590; MUID:90174930; PMID:2308831
A:Accession: S07594
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <MOR>
A:Cross-references: EMBL:X17095; NID:g59371; PIDN:CAA34953.1; PID:g59376
C:Genetics:
A:Map position: segment DNA1
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match      64.2%; Score 230; DB 2; Length 358;
Best Local Similarity 60.0%; Pred. No. 4e-19;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
DB 109 TVEWGFQIDGRSARGGQGSANDAYAKALNSGSKSEALNVIRELVPKDFVLOFHNLSNL 168

QY 61 DRIEDKTPPE 70
DB 169 DRIFQEPAP 178

RESULT 4
JQ1887
AL1 protein - tomato yellow leaf curl virus (strain Australia)
N:Alternate names: C1 protein
C:Species: tomato yellow leaf curl virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999
C:Accession: JQ1887
R:Dry, I.B.; Rigden, J.E.; Krake, L.R.; Mullineaux, P.M.; Rezaian, M.A.
J. Gen. Virol. 74, 147-151, 1993
A:Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.
A:Reference number: JQ1885; MUID:93139778; PMID:8423446
A:Accession: JQ1887
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <DRY>
A:Cross-references: GB:S53251
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match      62.0%; Score 222; DB 1; Length 362;
Best Local Similarity 52.9%; Pred. No. 3.5e-18;
Matches 45; Conservative 9; Mismatches 15; Indels 16; Gaps 1;

QY 1 TLVWGEFQVDRSGRGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
DB 110 TLEWGFQIDGRSARGGQGSANDAYAAQALNTGSKSEALNVIRELAPKDYVLOFHNLSNL 169

QY 61 DRI-----FDKTPPE 69
|||
|||
```

```
DB 170 DRIFTPPLEVTVSPFLSSSFDVRPE 194

RESULT 5
QOCVM1
AV1 protein - abutilon mosaic virus (isolate West India)
C:Species: abutilon mosaic virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Apr-1994
C:Accession: A36214
R:Frischmuth, T.; Zimmatt, G.; Jeske, H.
Virology 178, 461-468, 1990
A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as we
A:Reference number: A36214; MUID:91020984; PMID:2219703
A:Accession: A36214
A:Molecule type: DNA
A:Residues: 1-355 <FRI>
A:Cross-references: EMBL:X15983
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match      60.6%; Score 217; DB 1; Length 355;
Best Local Similarity 58.6%; Pred. No. 1.3e-17;
Matches 41; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
DB 110 TAEWGEFQIDGRSARGGQQTANDSYAKALNAGDVQSALNILEEQPKDYVLOFHNLSNL 169

QY 61 DRIEDKTPPE 70
DB 170 ERIFAKAPEP 179

RESULT 6
JQ2300
replicase - pepper huasteco virus (component A)
N:Alternate names: ORF AL1 protein
C:Species: pepper huasteco virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Sep-1999
C:Accession: JQ2300
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Herrera-Estrella, L.; Rivera-Bustamante, R.
J. Gen. Virol. 74, 2225-2231, 1993
A:Title: Complete nucleotide of pepper huasteco virus: Analysis and comparison with b1f
A:Reference number: JQ2299; MUID:94015007; PMID:8409944
A:Accession: JQ2300
A:Molecule type: DNA
A:Residues: 1-349 <TOR>
A:Cross-references: GB:X70418; NID:961023; PIDN:CAA49856.1; PID:g61025
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match      60.3%; Score 216; DB 2; Length 349;
Best Local Similarity 58.6%; Pred. No. 1.7e-17;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGQTSNDAAAALAAASSAAALQIIREKIPEKYLFOFHNLSNL 60
DB 110 TVEWGEFQIDGRSARGGQGSANDTYAKALNSASAEALQIIEEQPKDFLOFHNVSNA 169

QY 61 DRIEDKTPPE 70
DB 170 NRIFQTPPEP 179

RESULT 7
S31875
AL1 protein - pepper rizado amarillo virus
C:Species: pepper rizado amarillo virus
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 20-Sep-1999
C:Accession: S31875
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera-E
submitted to the EMBL Data Library, February 1993
A:Description: Complete nucleotide sequence of pepper huasteco virus: analysis and comp
```



A;Reference number: S31872  
A;Accession: S31875  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-349 <TOR>  
A;Cross-references: EMBL:X70418; NID:g61023; PIDN:CAA49856.1; PID:g61025  
A;Note: the source is designated as pepper huasteco virus  
C;Superfamily: tomato golden mosaic virus All protein

Query Match 60.3%; Score 216; DB 2; Length 349;  
Best Local Similarity 58.6%; Pred. No. 1.7e-17;  
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60  
DB 110 TLVGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 169  
QY 61 DRIFDKTPEP 70  
DB 170 NRIFQTPPEP 179

RESULT 8  
S39211  
gene C1 protein - tomato yellow leaf curl virus  
C;Species: tomato yellow leaf curl virus  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Sep-1999  
C;Accession: S39211  
R;Noris, E.; Hidalgo, E.; Accotto, G.; Moriones, E.  
submitted to the EMBL Data Library, August 1993  
A;Description: High similarity among the tomato yellow leaf curl virus isolates from the  
A;Reference number: S39209  
A;Accession: S39211  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-359 <NOR>  
A;Cross-references: EMBL:Z25751; NID:g433655; PIDN:CAA81026.1; PID:g433658  
C;Superfamily: tomato golden mosaic virus All protein

Query Match 60.3%; Score 216; DB 2; Length 359;  
Best Local Similarity 58.0%; Pred. No. 1.8e-17;  
Matches 40; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVWGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 61  
DB 111 LVWGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 170  
QY 62 RIFDKTPEP 70  
DB 171 RVFQVPPAP 179

RESULT 9  
JQ1870  
All protein - tomato mottle virus (isolate Florida)  
C;Species: tomato mottle virus  
C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 07-May-1999  
C;Accession: JQ1870  
R;Abouzaïd, A.M.; Polston, J.E.; Hiebert, E.  
J. Gen. Virol. 73, 3225-3229, 1992  
A;Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated from  
A;Reference number: JQ1869; MUID:93107858; PMID:1469361  
A;Accession: JQ1870  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-358 <ABO>  
A;Cross-references: GB:I14460  
C;Genetics:  
A;Map position: segment A  
C;Superfamily: tomato golden mosaic virus All protein

Query Match 59.8%; Score 214; DB 1; Length 358;  
Best Local Similarity 55.7%; Pred. No. 3e-17;

Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 60  
DB 107 TLVGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 166  
QY 61 DRIFDKTPEP 70  
DB 167 ERIFAKAPEP 176

RESULT 10  
JQ2327  
All protein - Indian cassava mosaic virus  
N;Alternate names: replication-associated protein  
C;Species: Indian cassava mosaic virus  
C;Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 20-Sep-1999  
C;Accession: JQ2327; S35883  
R;Hong, Y.G.; Robinson, D.J.; Harrison, B.D.  
J. Gen. Virol. 74, 2437-2443, 1993  
A;Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-tr  
A;Reference number: JQ2326; MUID:94065670; PMID:8245859  
A;Accession: JQ2327  
A;Molecule type: DNA  
A;Residues: 1-351 <HON>  
A;Cross-references: EMBL:Z24758; NID:g395351; PIDN:CAA80891.1; PID:g584046  
C;Superfamily: tomato golden mosaic virus All protein

Query Match 59.5%; Score 213; DB 2; Length 351;  
Best Local Similarity 61.2%; Pred. No. 3.8e-17;  
Matches 41; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 4 WGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 63  
DB 113 WGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 172  
QY 64 FDKTPEP 70  
DB 173 FTRPPPP 179

RESULT 11  
S22593  
hypothetical protein C4 - tomato yellow leaf curl virus  
C;Species: tomato yellow leaf curl virus  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Sep-1999  
C;Accession: S22593  
R;Kheyr-Pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, I.  
Nucleic Acids Res. 19, 6763-6769, 1991  
A;Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopar  
A;Reference number: S22588; MUID:92107660; PMID:1840676  
A;Accession: S22593  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-359 <KHE>  
A;Cross-references: EMBL:X61153; NID:g62211; PIDN:CAA43466.1; PID:g62217  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991  
C;Superfamily: tomato golden mosaic virus All protein

Query Match 59.2%; Score 212; DB 2; Length 359;  
Best Local Similarity 56.5%; Pred. No. 5.2e-17;  
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVWGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 61  
DB 111 LVWGEFQVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPEKYLQFHNLSNL 170  
QY 62 RIFDKTPEP 70  
DB 171 RVFQVPPAP 179

RESULT 12

```

A;Residues: 1-359 <CRE>
A;Cross-references: EMBL:Z28390; NID:G1041671; PID:G1334964
C;Superfamily: tomato golden mosaic virus All protein

Query Match      56.7%; Score 203; DB 2; Length 359;
Best Local Similarity 53.6%; Pred. No. 5.8e-16;
Matches 37; Conservative 12; Mismatches 20; Indels 0; Gaps 0;

QY  2  LVNGEFOVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNLD 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  111 LEWGTFOIDGRSARGGQQTANDAYAKAINARSKSEALDVIKQAPRDYVLHFNLSNLD 170
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  62 RIFDKTPEP 70
    :|||:|||||
Db  171 KVFQVPPAP 179

RESULT 15
QQCVCI
All protein - tomato yellow leaf curl virus
N;Alternate names: CI protein
C;Species: tomato yellow leaf curl virus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: D40779
R;Navot, N.; Pichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.
Virology 185, 151-161, 1991
A;Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single
A;Reference number: A40779; MUID:92024070; PMID:1926771
A;Accession: D40779
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-357 <NAV>
A;Cross-references: GB:X15656; NID:G62204; PIDN:CAA33688.1; PID:G62207
C;Superfamily: tomato golden mosaic virus All protein

Query Match      53.1%; Score 190; DB 1; Length 357;
Best Local Similarity 60.7%; Pred. No. 1.9e-14;
Matches 37; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY  4  WGFEFOVDRSARGGCOTSDNDAALAAASSAAALQIIREKIPKYLQFHNLSNLDRI 63
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  111 FGVSQIDGRSARGGQQSANDAYAEALNSGSKSEALNLTKEKAPKQYILQFHNLSNLDRI 170
    64 P 64
    171 P 171

Search completed: December 23, 2003, 09:05:19
Job time : 12 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds  
(without alignments)  
569.747 Million cell updates/sec

Title: US-09-289-346b-3  
Perfect score: 358  
Sequence: 1 TLVWGFQVDRSGCGCQT.....FQFHNLSNLDRIFDKTPPEP 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	92.7	352	1	VAL1_TGMV
2	243	67.9	361	1	VAL1_PYMV
3	230	64.2	358	1	VAL1_CLVK
4	230	64.2	358	1	VAL1_CLVN
5	222	62.0	362	1	VAL1_TYLC
6	217	60.5	355	1	VAL1_ABMV
7	216	60.3	349	1	VAL1_PHV
8	216	60.3	359	1	VAL1_TYLCU
9	215	60.1	353	1	VAL1_BGMV
10	214	59.8	361	1	VAL1_TMOV
11	212	59.2	359	1	VAL1_TYLCM
12	208	58.1	358	1	VAL1_BCTV
13	190	53.1	357	1	VAL1_TYLCV
14	115	32.1	347	1	VAL1_SLVC
15	70.5	19.7	466	1	SP8H_HUMAN
16	70.5	19.7	486	1	SP8H_MOUSE
17	69	19.3	577	1	T2FA_DROME
18	66	18.4	207	1	IL6_MARMO
19	66	18.4	508	1	CROC_DROME
20	65	18.2	671	1	EMOC_DROME
21	62.5	17.5	1077	1	HLES_DROME
22	60.5	16.9	829	1	E74A_DROME
23	60.5	16.9	883	1	E74B_DROME
24	60	16.8	314	1	PMXB_HUMAN
25	60	16.8	314	1	PMXB_MOUSE
26	59.5	16.6	470	1	RHBA_RHME
27	59	16.5	379	1	CYB_ASTPE
28	59	16.5	498	1	CALR_PIG
29	59	16.5	513	1	HEMO_CHICK
30	59	16.5	3591	1	PHAB_BORPE
31	58.5	16.3	297	1	MEL_DROME
32	58.5	16.3	478	1	RDPI_SCHPO
33	58.5	16.3	1264	1	MOLR_ECOLI

```

34 58.5 16.3 1713 1 LWA3_HUMAN
35 58 16.2 732 1 CYG4_HUMAN
36 58 16.2 1081 1 UL52_HSVB
37 58 16.2 1992 1 TRIB_HUMAN
38 57.5 16.1 303 1 ALB3_MAIZE
39 57.5 16.1 338 1 HXDB_HUMAN
40 57.5 16.1 557 1 SASB_ANAPL
41 57.5 16.1 593 1 DR11_HUMAN
42 57.5 16.1 601 1 DR11_MOUSE
43 57.5 16.1 1556 1 PROS_DROVI
44 57 15.9 387 1 VE2_HPV41
45 57 15.9 401 1 HME1_MOUSE

```

## ALIGNMENTS

```

RESULT 1
VAL1_TGMV
ID VAL1_TGMV STANDARD; PRT; 352 AA.
AC P03567;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DB AL1 protein.
GN ACl.
OS Tomato golden mosaic virus (TGMV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10831;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;
RT "Complete nucleotide sequence of the infectious cloned DNA components
RT of tomato golden mosaic virus: potential coding regions and regulatory
RT sequences."
RL EMBO J. 3:2197-2205(1984).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
CC EMBL; K02029; -; NOT ANNOTATED_CDS.
DR PIR; A04170; QCCVLI.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOTALI.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 223 230 ATP (POTENTIAL).
SQ SEQUENCE 352 AA; 40332 MW; C3C938E9644B44 CRC64;

Query Match 92.7%; Score 332; DB 1; Length 352;
Best Local Similarity 92.9%; Pred. No. 1.2e-31;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGCGCQTSDAAALAAALAAALAAALQIREKIPKYLQFPHNLSNL 60
Db 111 TLVWGFQVDRSGCGCQTSDAAALAAALAAALAAALQIREKIPKYLQFPHNLSNL 170

QY 61 DRIFDKTPPEP 70
Db 171 DRIFDKTPPEP 180

RESULT 2
VAL1_PYMV
ID VAL1_PYMV STANDARD; PRT; 361 AA.
AC P27258;

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DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC
CC EMBL; D00940; BAA00782.1; -.
DR F1R; J00364; Q0CVPT.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;

Query Match 67.9%; Score 243; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 3.8e-21;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGCGQTSNDAAAALQIIRKIPKYLQFQHNLSNL 60
DB 110 TLWGLFQIDGRSARGCGQTVNDAAAALNSGKTEAMKIKELPEKLFQVHNSL 169
QY 61 DRIFDKTPE 69
DB 170 DRIFDKAPE 178

RESULT 3
VAL1_CLVN STANDARD; PRT; 358 AA.
AC P149E2;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
KW AC1.
FT NP_BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;

Query Match 67.9%; Score 243; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 3.8e-21;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGCGQTSNDAAAALQIIRKIPKYLQFQHNLSNL 60
DB 110 TLWGLFQIDGRSARGCGQTVNDAAAALNSGKTEAMKIKELPEKLFQVHNSL 169
QY 61 DRIFDKTPE 69
DB 170 DRIFDKAPE 178
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CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753BE92D69 CRC64;

Query Match 64.2%; Score 230; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 1.3e-19;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGCGQTSNDAAAALQIIRKIPKYLQFQHNLSNL 60
DB 109 TVWGGQFQIDGRSARGCGQSANDAYAKALNSGKSEALNVIRELVKDFVLQFQHNLSNL 168
QY 61 DRIFDKTPE 70
DB 169 DRIFQPPAP 178

RESULT 4
VAL1_CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
KW AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
R Nucleic Acids Res. 18:197-198(1990).
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CC
CC EMBL; X17095; CAA34953.1; -.
DR F1R; S07594; S07594.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16BB0CB2D5E2C CRC64;

Query Match 64.2%; Score 230; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 1.3e-19;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGCGQTSNDAAAALQIIRKIPKYLQFQHNLSNL 60
DB 109 TVWGGQFQIDGRSARGCGQSANDAYAKALNSGKSEALNVIRELVKDFVLQFQHNLSNL 168
QY 61 DRIFDKTPE 70
DB 169 DRIFQPPAP 178
```

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EMBL; X15983; -; NOT_ANNOTATED_CDS.
PIR; A36214; QOCVWL.
InterPro; IPR001191; Gemini_AL1.
Pfam; PF00799; Gemini_AL1; 1.
PRINTS; PR00227; GEMCOATALL.
ProDom; PD000736; Gemini_AL1; 1.
ATP-binding.
NP_BIND 221 228 ATP (POTENTIAL).
SEQUENCE 355 AA; 40257 MW; 16A2C8A63251E95 CRC64;

Query Match 60.6%; Score 217; DB 1; Length 355;
Best Local Similarity 58.6%; Pred. No. 4.3e-18;
Matches 41; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 TLWGFEQVDGRSGCGQTSDNDAAAALASSAAALOITREKIPEKYLFOFHNLSNL 60
DB : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
110 TAEWGEFDIGRSARGGQQGTANDSYAKALNAGDVQSALNLIKKEPKQDYVLQNHRISNL 169

QY 61 DRIFDKTPEP 70
DB : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
170 ERIFAKAPEP 179

RESULT 7
IID VAL1 PHUV STANDARD; PRT; 349 AA.
AC Q06923;
DDT 01-JUN-1994 (Rel. 29, Created)
DDE 01-JUN-1994 (Rel. 29, Last sequence update)
DDE 01-JUN-1994 (Rel. 29, Last annotation update)
DDE AL1 protein.
OS AL1.
GN Pepper huasteco virus (PHV).
NCBI_FaxID=28349;
OX Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
RN [1]
RR SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Bacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
RT comparison with bipartite Geminiviruses.";
RL J. Gen. Virol. 74:2225-2231(1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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-----
EMBL; X70418; CAA49856.1; -.
PIR; JQ2300; JQ2300.
DR PIR; S31875; S31875.
InterPro; IPR001191; Gemini_AL1.
Pfam; PF00799; Gemini_AL1; 1.
PRINTS; PR00227; GEMCOATALL.
ProDom; PD000736; Gemini_AL1; 1.
ATP-binding.
NP_BIND 221 228 ATP (BY SIMILARITY).
SEQUENCE 349 AA; 39722 MW; D5FAE76CD56370F4 CRC64;

Query Match 60.3%; Score 216; DB 1; Length 349;
Best Local Similarity 58.6%; Pred. No. 5.5e-18;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLWGFEQVDGRSGCGQTSDNDAAAALASSAAALOITREKIPEKYLFOFHNLSNL 60
DB : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
110 TVEWGEFDIGRSARGGQQGSANDTYAKALNSAEALQITKEPOQHFFLOFHNVSNA 169

QY 61 DRIFDKTPEP 70

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Db      170 NRIFQTPPEP 179
      :|||
      :|||
      :|||

RESULT 8
VAL1_TYLCU
ID VAL1_TYLCU STANDARD; PRT; 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE All protein (Cl protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=371139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Norris E., Hidaigo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
RT from the west Mediterranean basin: the nucleotide sequence of an
RT infectious clone from Spain.";
RL Arch. Virol. 135:165-170(1994).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
CC -----
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CC -----
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=371139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Norris E., Hidaigo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
RT from the west Mediterranean basin: the nucleotide sequence of an
RT infectious clone from Spain.";
RL Arch. Virol. 135:165-170(1994).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
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CC -----
DR EMBL; Z25751; CAA81026.1; -.
DR PIR; S39211; S39211.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3EC CRC64;

Query Match 60.3%; Score 216; DB 1; Length 359;
Best Local Similarity 58.0%; Pred. No. 5.7e-18;
Matches 40; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVWGEFQVDRSARGGCGQTSNDAAAALAAASSAAALQIIREKIPKYLFOHNLNSLD 61
Db 111 LEWGTQFIDGRSARGGCGQQTANDAYAKAINAGSKSEALDWIKELAPRDYILHFNHNSLD 170
QY 62 RIFDKTPEP 70
Db 171 RVFQVPPAP 179

Query Match 60.3%; Score 216; DB 1; Length 359;
Best Local Similarity 58.0%; Pred. No. 5.7e-18;
Matches 40; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVWGEFQVDRSARGGCGQTSNDAAAALAAASSAAALQIIREKIPKYLFOHNLNSLD 61
Db 111 LEWGTQFIDGRSARGGCGQQTANDAYAKAINAGSKSEALDWIKELAPRDYILHFNHNSLD 170
QY 62 RIFDKTPEP 70
Db 171 RVFQVPPAP 179

RESULT 9
VAL1_BGMV
ID VAL1_BGMV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE All protein (40.2 kDa protein).
GN AC1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Howarth A.J., Caton J., Bossert M., Goodman R.M.;
RT "Nucleotide sequence of bean golden mosaic virus and a model for gene

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RT regulation in geminiviruses.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; M10070; AAA46318.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 60.1%; Score 215; DB 1; Length 353;
Best Local Similarity 58.6%; Pred. No. 7.3e-18;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLWGEFQVDRSARGGCGQTSNDAAAALAAASSAAALQIIREKIPKYLFOHNLNSNL 60
Db 110 TIWGEFQVDRSARGGCGQTSNDAAAALAAASSAAALQIIREKIPKYLFOHNLNSNL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFPKVPEP 179

RESULT 10
VAL1_TMOV
ID VAL1_TMOV STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE All protein.
GN All.
OS Tomato mottle virus (isolate Florida) (TMov).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93107858; PubMed=1469361;
RA Abouzid A.M., Polston J.E., Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida.";
RL J. Gen. Virol. 73:3225-3229(1992).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; L14460; AAC32414.1; -.
DR PIR; J01870; J01870.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 8138865CEAC6950 CRC64;

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01-APR-1990 (Rel. 14, Last sequence update)  
01-AUG-1992 (Rel. 23, Last annotation update)  
AL1 protein (40.8 kDa protein).  
Beet curly top virus (BCTV).  
Viruses; ssDNA viruses; Geminiviridae; Curtovirus.  
NCBI\_TaxID=10840;  
[1]  
SEQUENCE FROM N.A.  
Stanley J., Martham P.G., Callis R.J., Pinner M.S.;  
"The nucleotide sequence of an infectious clone of the geminivirus  
beet curly top virus.";  
EMBO J. 5:1761-1767(1986).  
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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EMBL; X04144; -; NOT ANNOTATED CDS.  
InterPro: IPR001191; Gemini\_AL1.  
Pfam: PF00799; Gemini\_AL1; 1.  
PRINTS: PR00227; GENCOATALL1.  
ProDom: PD000736; Gemini\_AL1; 1.  
ATP-binding.  
NP BIND 222 229 ATP (POTENTIAL).  
Query Match 358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;  
Best Local Similarity 58.1%; Score 208; DB 1; Length 358;  
Matches 39; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Qy 1 TLVGEEFQDGSRARGGCQTSSNDAAAALAASAAALAIIREKIPFKYLPOFHNLNSL 60  
Db 110 TIENGFEQDGSARGGQQTTANSYAKALNATSLDQLQLIKKEQPXDYFLQHHLNNNA 169

Qy 61 DRIPDKTPPE 70  
Db 170 QKIFQRDPDP 179

RESULT 13  
VALI\_TYLCV  
ID VALI\_TYLCV STANDARD; PRT; 357 AA.  
AC P27259;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DE 01-JUN-1994 (Rel. 29, Last annotation update)  
DL Al1 protein (Cl protein).  
GN Cl.  
OS Tomato yellow leaf curl virus (TYLCV).  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
NCBI\_TaxID=10832;  
[1]  
RN MEDLINE=92024070; PubMed=1926771,  
RX Navot N., Fichersky E., Zeidan M., Zamir D., Czosek H.;  
RA "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus  
with a single genomic component.";  
RT Virology 185:151-161(1991).  
RL CC  
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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DR EMBL; X15656; CAA33688.1; -.
DR PIR; D40779; QQCVC1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1.1.
KW ATP-binding. 219 226 ATP (POTENTIAL).
FT NP_BIND 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match
Best Local Similarity 53.1%; Score 190; DB 1; Length 357;
Matches 37; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 4 WGEFQVDSRGCGQTSNDAAALAAASSAAALQIIRKIPKYLFOFHNLSNLDRI 63
Db 111 FGVSDIGRSARGGQSQSANDAYAEALNSGSKSEALNLKAPKAPDYILQFHNLSNLDRI 170

QY 64 F 64
Db 171 F 171

RESULT 14
VAL1 SLCV STANDARD; PRT; 347 AA.
AC P29018;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE AL1 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10829;
RN [1]_
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G., Lazdins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic components of a bipartite squash leaf curl geminivirus with a broad host range phenotype."
RT Virology 180:58-69 (1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
CC EMBL; M38183; AAC32410.1; ALT_INIT.
CC PIR; C36785; QQCVC1.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1.1.
CC PRINTS; PR00227; GEMCOATL1.
CC ProDom; PD000736; Gemini_AL1.1.
KW ATP-binding. 218 225 ATP (POTENTIAL).
FT NP_BIND 347 AA; 39110 MW; AFAABBDDE122110E CRC64;
SQ SEQUENCE 347 AA; 39110 MW; AFAABBDDE122110E CRC64;

Query Match
Best Local Similarity 32.1%; Score 115; DB 1; Length 347;
Matches 24; Conservative 14; Mismatches 24; Indels 4; Gaps 1;

QY 5 GEFQVDSRGCGQTSNDAAALAAASSAAALQIIRKIPKYLFOFHNLSNLDRI 64
Db 116 GQYKVSQ----GSKSNKDDVYHNAVNAAGSAGEALDIKAGDPKTFIVYHNLNANVERLF 171

QY 65 DKTPEP 70
Db 172 QKPEP 177

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RESULT 15
SP8H HUMAN STANDARD; PRT; 466 AA.
AC Q8IXZ3; Q96MJ1;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical sp-like zinc finger protein MGC41921/FLJ322295.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Prostate;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida H., Yamashita H., Chiba Y.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Maehuo Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]_
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green A.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RL Proc Natl Acad Sci U S A. 99:16899-16903 (2002).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8IXZ3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8IXZ3-2; Sequence=VSP_007441;
CC -1- SIMILARITY: BELONGS TO THE SP1 FAMILY OF C2H2-TYPE ZINC-FINGER
CC PROTEINS.
CC -1- SIMILARITY: Contains 3 C2H2-type zinc fingers.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-19 is the initiator.
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CC -----
CC EMBL; AK056857; BAB71297.1; -.
CC EMBL; BC038669; AAB38669.1; -.

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DR InterPro: IPR007087; Znf\_C2H2.  
DR Pfam: PF00096; zf-C2H2; 3.  
DR ProDom: PD000003; Znf\_C2H2; 1.  
DR SMART: SM00355; Znf\_C2H2; 3.  
DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 3.  
DR PROSITE: PS00157; ZINC\_FINGER\_C2H2\_2; 3.  
KW Hypothetical protein; Nuclear protein; Zinc-finger; Metal-binding;  
KW DNA-binding; Repeat; Alternative splicing.  
FT DOMAIN 29 132 SER-RICH.  
FT DOMAIN 86 99 ALA-RICH.  
FT ZN\_FING 332 356 C2H2-TYPE 1.  
FT ZN\_FING 362 386 C2H2-TYPE 2.  
FT ZN\_FING 392 414 C2H2-TYPE 3.  
FT VARSPLIC 111 124 Missing (in isoform 2).  
FT /FTid=VSP\_007441.  
FT CONFLICT 406 406 R -> H (IN REF. 1).  
SQ SEQUENCE 466 AA; 47079 MW; AD238C6C0A9D5401 CRC64;  
  
Query Match 19.7%; Score 70.5; DB 1; Length 466;  
Best Local Similarity 59.4%; Pred. No. 1;  
Matches 19; Conservative 3; Mismatches 7; Indels 3; Gaps 1;  
  
Qy 7 FQVDGRSARGCQTSNDAAAALAAASAAAAL 38  
Db 72 FGVSGASRNGG---SSSAAAAAAAAAAAAAAAAAL 100

Search completed: December 23, 2003, 08:57:37  
Job time : 7.7778 secs

Result No.	Query No.	Score	Query \$		Length	DB	ID	Description
			Match					
1	1	293	81.8	351	12	Q91R10	Q91r10	tomato save
2	2	291	81.3	352	12	Q9E000	Q9e000	tomato rugo
3	3	284	79.3	232	12	Q8QPV3	Q8qpv3	tomato chlo
4	4	276	77.1	226	12	Q9F727	Q09f727	leonurus mo
5	5	271	75.7	314	12	Q9EUT8	Q9e1t8	sweet potat
6	6	271	75.7	364	12	Q9Q855	Q9q855	sweet potat
7	7	267	73.7	226	12	Q9WHF6	Q9whf6	tomato mild
8	8	263	73.5	359	12	Q91M88	Q91m88	tobacco lea
9	9	263	73.5	359	12	Q8JVE8	Q8jve8	tomato curl
10	10	262	73.2	361	12	Q67574	Q67574	bean golden
11	11	260	72.6	149	12	P88975	P88975	macroptiliu
12	12	260	72.6	225	12	Q9QDB1	Q9qdb1	cowpea goi
13	13	250	72.6	233	12	Q9YL44	Q9yla4	macroptiliu
14	14	250	72.3	185	12	Q98693	Q98693	sida golden
15	15	251	71.8	360	12	Q8QMH4	Q8gmh4	sida mottle
16	16	255	71.2	361	12	Q8QVH0	Q8gvh0	aceratrum en

```
RESULT 2
Q9E000
ID Q9E000 PRELIMINARY; PRT; 352 AA.
AC Q9E000;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE Replication-associated protein.
GN AC1.
OS Tomato rugose mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=134599;
RN [1]
RP SEQUENCE FROM N.A.
RA Fernandes J.J., Fontes E.P.B., Brommonschenkel S.H., Carvalho M.G.,
RA Zambolim E.M., Zerbini F.M.;
RT "Molecular Cloning and Characterization of Tomato rugose mosaic virus
RT (TRMV), a Begomovirus Isolated from Tomatoes at Triangulo Mineiro,
RT Minas Gerais, Brazil.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF291705; AAG15546.1; -.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini AL1; 1.
SQ SEQUENCE 352 AA; 40012 MW; 47CD55838E24D613 CRC64;

Query Match 81.3%; Score 291; DB 12; Length 352;
Best Local Similarity 78.6%; Pred. No. 7.9e-26;
Matches 55; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQDGRSARGGQTSNDAAAALAAASSAAALQIIREKIPEKLFQFHNLSNL 60
Db 111 TLVWGEFQDGRSARGGQTSNDAAAALAAASSAAALQIIREKMPKLFQFHNLSNL 170

QY 61 DRIFDKTPEP 70
Db 171 DRIFARAPEP 180

RESULT 3
Q8QPV3
ID Q8QPV3 PRELIMINARY; PRT; 232 AA.
AC Q8QPV3;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Tomato chlorotic vein virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172390;
RN [1]
RP SEQUENCE FROM N.A.
RA Ribeiro S.G., Ambrozavicius L.P., de Avila A.C., Calegario R.F.,
RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049205; AAL82824.1; -.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; I.
DR ProDom; PD000736; Gemini AL1; 1.
FT NON_TER 232
SQ SEQUENCE 232 AA; 26319 MW; 254CASD040D35DDA CRC64;

Query Match 79.3%; Score 284; DB 12; Length 232;
Best Local Similarity 77.1%; Pred. No. 3.2e-25;
Matches 54; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQDGRSARGGQTSNDAAAALAAASSAAALQIIREKIPEKLFQFHNLSNL 60
Db 111 TLVWGEFQDGRSARGGQTSNDAAAALAAASSAAALQIIREKMPKLFQFHNLSNL 170

RESULT 4
O09727
ID O09727 PRELIMINARY; PRT; 226 AA.
AC O09727;
DT 01-JUL-1997 (TREMELrel. 04, Created)
DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN REP.
OS Leonurus mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=58177;
RN [1]
RP SEQUENCE FROM N.A.
RA Faria J.C., Maxwell D.P.;
RT "Variability in geminivirus associated with Phaseolus vulgaris in
RT Brazil.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U92532; AAB51157.1; -.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini AL1; 1.
FT NON_TER 226
SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;

Query Match 77.1%; Score 276; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 2.7e-24;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQDGRSARGGQTSNDAAAALAAASSAAALQIIREKIPEKLFQFHNLSNL 60
Db 111 TLVWGEFQDGRSARGGQTSNDAAAALAAASSAAALQIIREKMPKLFQFHNLSNL 170

QY 61 DRIFDKTPEP 70
Db 171 DRIFAKAPEP 180

RESULT 5
Q9ELT8
ID Q9ELT8 PRELIMINARY; PRT; 314 AA.
AC Q9ELT8;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Replication association protein.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288227; AAG01006.1; -.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR
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DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 75.7%; Score 271; DB 12; Length 314;
Best Local Similarity 79.4%; Pred. No. 1.8e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGEFQVQDGRSARGGCQTSNDAAAAAALAAASAAAAALQIIREKIPEKYLQFHNLSNL 60
Ddb 110 TITWGEFQVQDGRSARGGCQQTANDAAALNAGSKEAALQIIREKLPEKYLQFHNLSNL 169
|||
QY 61 DRIFDKTP 68
Ddb 170 DRIFSPPP 177
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RESULT 6
Q9Q855 PRELIMINARY; PRT; 364 AA.
ID Q9Q855 AC Q9Q855;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Replication initiation protein Acl.
OS AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=100755;
RX [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RT virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0(1999).
DR EMBL; AF104036; AAD47173.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 75.7%; Score 271; DB 12; Length 364;
Best Local Similarity 79.4%; Pred. No. 1.8e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGEFQVQDGRSARGGCQTSNDAAAAAALAAASAAAAALQIIREKIPEKYLQFHNLSNL 60
Ddb 110 TITWGEFQVQDGRSARGGCQQTANDAAALNAGSKEAALQIIREKLPEKYLQFHNLSNL 169
|||
QY 61 DRIFDKTP 68
Ddb 170 DRIFSPPP 177
|||

RESULT 7
Q9WHF6 PRELIMINARY; PRT; 226 AA.
ID Q9WHF6 AC Q9WHF6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Replication-associated protein (Fragment).
OS REP.
OS Tomato mild mottle geminivirus.
OC Viruses; ssDNA viruses; Geminiviridae; unclassified Geminiviridae.
NCBI_TaxID=92943;
RX [1]

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DE CI protein.
OS Tomato curly stunt virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=128941;
RN [1]
RP SEQUENCE FROM N.A.
RA Pieterse G., Idris A.M., Kruger K., Brown J.K.;
RT "Tomato curly stunt virus, a new Begomovirus of tomato within TYLCV-Is
cluster in South Africa.";
RL Plant Dis. 84:810-810(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Pieterse G., Idris A.M., Kruger K., Brown J.K.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF261885; AAM80474.1; -
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 359 AA; 40715 MW; 751159837A87FDDC CRC64;

Query Match 73.5%; Score 263; DB 12; Length 359;
Best Local Similarity 70.0%; Pred. No. 1.6e-22;
Matches 49; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGCGQTSNDAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 60
Db 110 TLEWGFQVDSARGCGQTSNDAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 60
QY 61 DRIFDKTPEP 70
Db 170 DRIFQAPPEP 179

RESULT 10
Q67574
ID Q67574 PRELIMINARY; PRT; 361 AA.
AC Q67574;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Putative replicative protein.
GN AL1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration.";
RL Phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RT "Differentiation of bean-infecting geminiviruses by nucleic acid
RT hybridization probes and aspects of bean golden mosaic in Brazil.";
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus.";
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M88686; AAA46312.1; -
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.

SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 73.2%; Score 262; DB 12; Length 361;
Best Local Similarity 73.1%; Pred. No. 2.1e-22;
Matches 49; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 4 WGSFQVDSARGCGQTSNDAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 63
Db 113 WGHFQVDSARGCGQTSNDAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 172
QY 64 FDKTPEP 70
Db 173 FTKAPDP 179

RESULT 11
P88975
ID P88975 PRELIMINARY; PRT; 149 AA.
AC P88975;
DT 01-MAY-1997 (T-EMBLrel. 03, Created)
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
DT 01-MAY-2003 (T-EMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN ACl.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
RN [1]
RP SEQUENCE FROM N.A.
RA Roye M.E.;
RL Thesis (1996), Biochemistry, University of the West Indies, Jamaica.
DR EMBL; U75278; AAB36919.1; -
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 1 149
SQ SEQUENCE 149 AA; 16785 MW; E4CF5EDD4C9CD508 CRC64;

Query Match 72.6%; Score 260; DB 12; Length 149;
Best Local Similarity 68.6%; Pred. No. 1.3e-22;
Matches 48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGCGQTSNDAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 60
Db 52 TLEWGFQVDSARGCGQTSNDAAALAAASSAAALQIIRKIPKYLQFQHNLSNL 111
QY 61 DRIFDKTPEP 70
Db 112 DRIFMKDPEP 121

RESULT 12
Q9QDB1
ID Q9QDB1 PRELIMINARY; PRT; 225 AA.
AC Q9QDB1;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Cowpea golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1]
RP SEQUENCE FROM N.A.
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RT Brazil.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AF189708, AAF06318.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; I.
DR PRINTS: PR00227; GEMCOATALL1.
DR ProDom: PD000736; Gemini_AL1; 1.
FT NON_TER 225 225
SQ SEQUENCE 225 AA; 25766 MW; 1089CB6BD8D15B5D CRC64;

Query Match 72.6%; Score 260; DB 12; Length 225;
Best Local Similarity 73.1%; Pred. No. 2e-22;
Matches 49; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 4 WGFQVQDGRSARGCGCOTSDNAAAALAAASAAALQIIRKIPKYLFOFHNLSNLDRI 63
DB 113 WGFQVQDGRSARGCGCOTSDNAAAALAAASAAALQIIRKIPKYLFOFHNLSNLDRI 172

QY 64 FDKTPEP 70
DB 173 FKPPPEP 179

RESULT 13
Q9YL44 PRELIMINARY; PRT; 233 AA.
AC Q9YL44;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Macrotidium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
RN [1]
RC STRAIN=Jamaica strain 1;
RA Roye M.E.;
RT "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RC STRAIN=Jamaica strain 1;
RA Roye M.E.;
RT "Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF098940; AAD17850.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; I.
DR PRINTS: PR00227; GEMCOATALL1.
DR ProDom: PD000736; Gemini_AL1; 1.
FT NON_TER 233 233
SQ SEQUENCE 233 AA; 26356 MW; AA490AF4D2166A02 CRC64;

Query Match 72.6%; Score 260; DB 12; Length 233;
Best Local Similarity 68.6%; Pred. No. 2.1e-22;
Matches 48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGFQVQDGRSARGCGCOTSDNAAAALAAASAAALQIIRKIPKYLFOFHNLSNLDRI 60
DB 110 TIWGVFQIDGRSARGCGCOTSDNAAAALAAASAAALQIIRKIPKYLFOFHNLSNLDRI 169

QY 61 DRIFDKTPEP 70
DB 170 DRIFDKTPEP 179

RESULT 14
Q98693 PRELIMINARY; PRT; 185 AA.
ID Q98693
AC Q98693;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)

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DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RC STRAIN=Jamaica;
RA Roye M.E.; McLaughlin W.A., Nakula N.K., Maxwell D.P.;
RT "Genetic diversity among geminiviruses associated with the weed species Sida spp. Macrotidium lathyroides, and Wissadula amplissima from Jamaica.";
RL Plant Dis. 81:1251-1258 (1997).
DR EMBL: U67926; AAB97865.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; I.
DR PRINTS: PR00227; GEMCOATALL1.
DR ProDom: PD000736; Gemini_AL1; 1.
FT NON_TER 185 185
SQ SEQUENCE 185 AA; 20975 MW; 3913850A025A5BE1 CRC64;

Query Match 72.3%; Score 259; DB 12; Length 185;
Best Local Similarity 68.6%; Pred. No. 2.1e-22;
Matches 48; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGFQVQDGRSARGCGCOTSDNAAAALAAASAAALQIIRKIPKYLFOFHNLSNLDRI 60
DB 89 TIWGVFQIDGRSARGCGCOTSDNAAAALAAASAAALQIIRKIPKYLFOFHNLSNLDRI 148

QY 61 DRIFDKTPEP 70
DB 149 DRIFDKTPEP 158

RESULT 15
Q8QMH4 PRELIMINARY; PRT; 360 AA.
ID Q8QMH4
AC Q8QMH4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication associated protein Rep.
GN AC1.
OS Sida mottle virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=191460;
RN [1]
RC STRAIN=Jamaica;
RA Fontes E.P.B.;
RT "Molecular cloning of Sida mottle virus: a new species of Begomovirus from Brazil.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RA Fernandes A.V., Mariano A.C., Galvao R.M., Zerbini F.M.,
RA Fontes E.P.B.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY090555; AAM12371.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; I.
DR ProDom: PD000736; Gemini_AL1; 1.
SQ SEQUENCE 360 AA; 41319 MW; IDE968E4215FC167 CRC64;

Query Match 71.8%; Score 257; DB 12; Length 360;
Best Local Similarity 74.6%; Pred. No. 7.9e-22;
Matches 50; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 4 WGFQVQDGRSARGCGCOTSDNAAAALAAASAAALQIIRKIPKYLFOFHNLSNLDRI 63
DB 114 WGFQVQDGRSARGCGCOTSDNAAAALAAASAAALQIIRKIPKYLFOFHNLSNLDRI 173

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Qy 64 PDKTPEP 70  
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Db 174 FLKAPPEP 180

Search completed: December 23, 2003, 09:03:35  
Job time : 26.3333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds  
(without alignments)  
340.128 Million cell updates/sec

Title: US-09-289-346B-4

Perfect score: 361

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361	100.0	70	21 AAB18680	Mutant peptide der
2	346	95.8	70	21 AAB18677	Peptide fragment f
3	346	95.8	356	21 AAB18687	Amino acid sequenc
4	338	93.6	70	21 AAB18685	Mutant peptide der
5	335	92.8	70	21 AAB18688	Mutant peptide der
6	334	92.5	70	21 AAB18692	Mutant peptide der
7	332	92.0	70	21 AAB18684	Mutant peptide der
8	332	92.0	70	21 AAB18690	Mutant peptide der
9	331	91.7	70	21 AAB18678	Mutant peptide der

10	331	91.7	70	21 AAB18686	Mutant peptide der
11	330	91.4	70	21 AAB18689	Mutant peptide der
12	328	90.9	70	21 AAB18691	Mutant peptide der
13	325	90.0	70	21 AAB18681	Mutant peptide der
14	324	89.8	70	21 AAB18683	Mutant peptide der
15	322	89.2	70	21 AAB18682	Mutant peptide der
16	314	87.0	70	21 AAB18679	Mutant peptide der
17	222	61.5	359	17 AAR88870	Sardinian tomato y
18	222	61.5	359	17 AAR88871	Sardinian tomato y
19	222	61.5	359	17 AAR88872	Sardinian tomato y
20	219	60.7	353	18 AAW34338	Bean golden mosaic
21	219	60.7	353	18 AAW34332	Bean golden mosaic
22	219	60.7	353	18 AAW34333	Bean golden mosaic
23	219	60.7	353	18 AAW34334	Bean golden mosaic
24	219	60.7	353	18 AAW34335	Bean golden mosaic
25	217	60.1	353	8 AAP70407	ORF 4 gene product
26	214	59.3	361	18 AAW34336	Tomato mottle viru
27	214	59.3	361	18 AAW34324	Tomato mottle viru
28	214	59.3	361	18 AAW34325	Tomato mottle viru
29	214	59.3	361	18 AAW34326	Tomato mottle viru
30	205.5	56.9	50	23 AAO22043	Retinoblastoma-bin
31	203.5	56.4	361	8 AAP70562	Product of ORF 4 f
32	200	55.4	357	18 AAW34329	Tomato yellow leaf
33	200	55.4	357	18 AAW34330	Tomato yellow leaf
34	200	55.4	357	18 AAW34331	Tomato yellow leaf
35	198	54.8	362	19 AAW56495	Tobacco leaf curl
36	192	53.2	357	18 AAW34337	Tomato yellow leaf
37	104	28.8	142	24 ABP58120	Tomato yellow leaf
38	65.5	18.1	512	19 AAW68473	HIV-1 strain YBF30
39	63.5	17.6	665	22 ABP70991	Drosophila melanog
40	61.5	17.0	183	21 AAG60400	Arabidopsis thalia
41	61.5	17.0	299	18 AAW55450	H. pylori ORF 02ae
42	61.5	17.0	1203	21 AAY83275	Candida albicans C
43	61.5	17.0	1203	21 AAY84814	Amino acid sequenc
44	61	16.9	483	22 AAG91343	C glutamicum prote
45	60.5	16.8	131	18 AAW34327	Tomato mottle viru

## ALIGNMENTS

### RESULT 1

AAB18680  
ID AAB18680 standard; peptide; 70 AA.

XX AAB18680;

DT 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX Ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 42 /note= "wild type residue replaced with Ala"

FT Misc-difference 43 /note= "wild type residue replaced with Ala"

FT Misc-difference 44 /note= "wild type residue replaced with Ala"

XX WO2000054573-A1.

XX 21-SRP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.



XX PA (UYNC-) UNIV NORTH CAROLINA STATE.  
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;  
XX DR WPI; 2000-618851/59.  
XX XX  
PT Transgenic plants with increased resistance to geminivirus infection  
PT comprise a nucleic acid construct containing a nucleic acid sequence  
PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
PT -  
XX  
PS Claim 52; Page 43-44; 73pp; English.  
XX  
CC The present sequence represents a mutant peptide, derived from a  
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
CC protein are used to produce transgenic plants. The mutation in AL1 is  
CC present in a ribosome binding region, and expression of mutant AL1  
CC protein imparts increased resistance to geminivirus infection in the  
CC plant. Mutant AL1 proteins are useful for producing plants having  
CC increased resistance or reduced sensitivity to a geminivirus such as  
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
CC virus, cotton leaf curl virus or beet curly top virus.  
XX  
SQ Sequence 70 AA;  
Query Match 100.0%; Score 361; DB 21; Length 70;  
Best Local Similarity 100.0%; Pred. No. 1.6e-39;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TLVWGEFQVDRSGRGCGTSDNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLSNL 60  
DB 1 TLVWGEFQVDRSGRGCGTSDNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70  
RESULT 2  
AAB18677  
ID AAB18677 standard; peptide; 70 AA.  
XX  
AC AAB18677;  
XX  
DT 22-JAN-2001 (first entry)  
XX  
DE Peptide fragment from Rep protein of TGMV (amino acids 110-179).  
XX  
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
KW ribosome binding region; resistance; geminivirus infection.  
XX  
OS Tomato golden mosaic virus.  
XX  
PN WO200054573-Al.  
XX  
PD 21-SEP-2000.  
XX  
PF 15-MAR-2000; 2000WO-US06759.  
XX  
PR 18-MAR-1999; 99US-0125004.  
PR 09-APR-1999; 99US-0289346.  
XX  
PA (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
PI Hanley-Bowdoin L, Orozco BM, Kong L;  
XX  
DR WPI; 2000-618851/59.

XX PT Transgenic plants with increased resistance to geminivirus infection  
PT comprise a nucleic acid construct containing a nucleic acid sequence  
PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
PT -  
XX  
PS Disclosure; Page 18; 73pp; English.  
XX  
CC The present sequence is derived from a geminivirus replication (Rep)  
CC protein, which is also known as AL1. AL1 binds double-stranded DNA,  
CC catalyzes cleavage and ligation of single-stranded DNA, and interacts  
CC with other viral and host proteins. Mutants of the AL1 protein are used  
CC to produce transgenic plants. The mutation in AL1 is present in a  
CC ribosome binding region, and expression of mutant AL1 protein imparts  
CC increased resistance to geminivirus infection in the plant. Mutant AL1  
CC proteins are useful for producing plants having increased resistance or  
CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,  
CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl  
CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato  
CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,  
CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or  
CC beet curly top virus.  
XX  
SQ Sequence 70 AA;  
Query Match 95.8%; Score 346; DB 21; Length 70;  
Best Local Similarity 95.7%; Pred. No. 1.5e-37;  
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TLVWGEFQVDRSGRGCGTSDNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLSNL 60  
DB 1 TLVWGEFQVDRSGRGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70  
RESULT 3  
AAB18687  
ID AAB18687 standard; peptide; 356 AA.  
XX  
AC AAB18687;  
XX  
DT 22-JAN-2001 (first entry)  
XX  
DE Amino acid sequence of a geminivirus replication protein of TGMV.  
XX  
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
KW ribosome binding region; resistance; geminivirus infection.  
XX  
OS Tomato golden mosaic virus.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 354  
FT /note= "unspecified amino acid"  
XX  
PN WO200054573-Al.  
XX  
PD 21-SEP-2000.  
XX  
PF 15-MAR-2000; 2000WO-US06759.  
XX  
PR 18-MAR-1999; 99US-0125004.  
PR 09-APR-1999; 99US-0289346.  
XX  
PA (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
PI Hanley-Bowdoin L, Orozco BM, Kong L;  
XX  
DR WPI; 2000-618851/59.  
XX  
PT Transgenic plants with increased resistance to geminivirus infection

comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant AL1 protein with a mutation in the Rb binding region

Disclosure: Page 47-48; 73pp; English.

The present sequence represents a geminivirus replication (Rep) protein, which is also known as AL1. AL1 binds double-stranded DNA, catalyses cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the AL1 protein are used to produce transgenic plants. The mutation in AL1 is present in a ribosome binding region, and expression of mutant AL1 protein imparts increased resistance to geminivirus infection in the plant. Mutant AL1 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.

```

AA      SQ   Sequence    356 AA;
Query Match          95.8%; Score 346; DB 21; Length 356;
Best Local Similarity 95.7%; Pred. No. 1.2e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 TLVWGFQVDGRSARGCGCQTSDNDAAEALNASKEEALQITAAAIPKYLTFQHNLNSNL 60
        |||||
Db      110 TLVWGFQVDGRSARGCGTSDNDAAEALNASKEEALQIIRKKIPKYLTFQHNLNSNL 169
        |||||

Qy      61 DRIFDKTPEP 70
        |||||
Db      170 DRIFDKTPEP 179

```

RESULT 4  
AAB18685  
ID AAB18685 standard; peptide; 70 AA.  
XX  
XX AAB18685;  
XX  
XX  
XX  
DT 22-JAN-2001 (first entry)  
XX  
XX  
DE Mutant peptide derived from amino acids 110-179 of Rep (Al1) protein.  
XX  
XX Geminivirus; replication protein; Rep protein; Al1; transgenic plant;  
KW ribosome binding region; resistance; geminivirus infection.

XX	Key	Location/Qualifiers
PH	Misc-difference 10	
FT		/note= "wild type residue replaced with Ala"
FT		
XX		
PN	WO200054573-Al.	

PT	encoding a mutant Aul1 protein with a mutation in the Rb binding region
PT	-
XX	
PS	Claim 53; Page 46; 73pp; English.
XX	
CC	The present sequence represents a mutant peptide, derived from a
CC	geminivirus replication (Rep) protein, also known as Aul1. Aul1 binds
CC	double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC	DNA, and interacts with other viral and host proteins. Mutants of the Aul1
CC	protein are used to produce transgenic plants. The mutation in Aul1 is
CC	present in a ribosome binding region, and expression of mutant Aul1
CC	protein imparts increased resistance to geminivirus infection in the
CC	plant. Mutant Aul1 proteins are useful for producing plants having
CC	increased resistance or reduced sensitivity to a geminivirus such as
CC	tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC	virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC	cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC	virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC	virus, cotton leaf curl virus or beet curly top virus.
XX	
SQ	Sequence 70 AA;

```

Query Match      93.6%; Score 338; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 1.6e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY      1 TLVWGFQVDCRSARGGQTSNDAAAEALNASSKEEALQIIAAAIPEKYLQFPHNLNSNL 60
        |||||
Db       1 TLVWGFQVAGRSARGGQTSNDAAAEALNASSKEEALQIREKIPEKYLQFPHNLNSNL 60
        |||||

QY      61 DRIFDKTPEP 70
        |||||
Db       61 DRIFDKTPEP 70
        |||||

```

RESULT 5	
AAB18688	
ID	AAB18688 standard; peptide; 70 AA.
XX	
XX	AAB18688;
XX	
XX	
22-JAN-2001	(first entry)
DT	
XX	
DE	Mutant peptide derived from amino acids 110-179 of Rep (All) protein.
XX	
XX	Geminivirus; replication protein; Rep protein; All; transgenic plant;
KW	ribosome binding region; resistance; geminivirus infection.
XX	

Key	Location/Qualifiers
PH	
FT	Misc-difference 19
FT	/note= "wild type residue replaced with Ala"
FT	
FT	Misc-difference 20
FT	/note= "wild type residue replaced with Ala"
FT	

(UTNC-) UNIV NORTH CAROLINA STATE.  
XX  
PI Hanley-Bowdoin L, Orozco BM, Kong L;  
XX  
XX  
DR WPI; 2000-618851/59.

PT Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence  
 FT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX  
 XX  
 PS Disclosure; Page 48; 73pp; English.

CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.

XX  
 XX Sequence 70 AA;

Query Match 92.8%; Score 335; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 4e-36;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGQTNDAAAEALNASSKEEALQIIAAAIPEKYLQFPHNLSNL 60  
 DB 1 TLVWGEFQVDRSGRGCGCAASNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLSNL 60

QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70

RESULT 6  
 AAB18692  
 ID AAB18692 standard; peptide; 70 AA.  
 AC AAB18692;  
 XX  
 XX 22-JAN-2001 (first entry)  
 DT  
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 DE  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 XX Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 XX Key Location/Qualifiers  
 FH Key  
 FT Misc-difference 66 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"  
 XX  
 XX WO200054573-Al.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX

PT Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 FT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX  
 XX  
 PS Disclosure; Page 50; 73pp; English.

CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.

XX  
 XX Sequence 70 AA;

Query Match 92.5%; Score 334; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 5.5e-36;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGQTNDAAAEALNASSKEEALQIIAAAIPEKYLQFPHNLSNL 60  
 DB 1 TLVWGEFQVDRSGRGCGQTNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLSNL 60

QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70

RESULT 7  
 AAB18684  
 ID AAB18684 standard; peptide; 70 AA.  
 AC AAB18684;  
 XX  
 XX 22-JAN-2001 (first entry)  
 DT  
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 DE  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 XX Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 XX Key Location/Qualifiers  
 FH Key  
 FT Misc-difference 7 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"  
 XX  
 XX WO200054573-Al.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX

XX Transgenic plants with increased resistance to geminivirus infection  
PT comprise a nucleic acid construct containing a nucleic acid sequence  
PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
PT -  
XX  
XX Claim 52; Page 45; 73pp; English.  
XX  
XX The present sequence represents a mutant peptide, derived from a  
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
CC protein are used to produce transgenic plants. The mutation in AL1 is  
CC present in a ribosome binding region, and expression of mutant AL1  
CC protein imparts increased resistance to geminivirus infection in the  
CC plant. Mutant AL1 proteins are useful for producing plants having  
CC increased resistance or reduced sensitivity to a geminivirus such as  
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
CC virus, cotton leaf curl virus or beet curly top virus.  
XX  
XX Sequence 70 AA;  
SQ  
Query Match 92.0%; Score 332; DB 21; Length 70;  
Best Local Similarity 92.9%; Pred. No. 1e-35;  
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEALQIIAAIPEKYLQFHNLSNL 60  
DB 1 TLVWGEAAVDGSRGCGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70  
RESULT 8  
AAB18690  
ID AAB18690 standard; peptide; 70 AA.  
XX  
AC AAB18690;  
XX  
XX 22-JAN-2001 (first entry)  
XX  
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
KW ribosome binding region; resistance; geminivirus infection.  
XX  
OS Synthetic.  
OS Tomato golden mosaic virus.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 27 /note= "wild type residue replaced with Ala"  
FT FT Misc-difference 30 /note= "wild type residue replaced with Ala"  
FT FT Misc-difference 30 /note= "wild type residue replaced with Ala"  
XX  
XX WO200054573-A1.  
XX  
XX 21-SEP-2000.  
XX  
XX 15-MAR-2000; 2000WO-US06759.  
XX  
XX 18-MAR-1999; 99US-0125004.  
XX 09-APR-1999; 99US-0289346.  
XX  
XX (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hanley-Bowdoin L, Orozco BM, Kong L;  
XX

DR WPI; 2000-618851/59.  
XX  
XX Transgenic plants with increased resistance to geminivirus infection  
PT comprise a nucleic acid construct containing a nucleic acid sequence  
PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
PT -  
XX  
XX Disclosure; Page 49; 73pp; English.  
XX  
XX The present sequence represents a mutant peptide, derived from a  
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
CC protein are used to produce transgenic plants. The mutation in AL1 is  
CC present in a ribosome binding region, and expression of mutant AL1  
CC protein imparts increased resistance to geminivirus infection in the  
CC plant. Mutant AL1 proteins are useful for producing plants having  
CC increased resistance or reduced sensitivity to a geminivirus such as  
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
CC virus, cotton leaf curl virus or beet curly top virus.  
XX  
XX Sequence 70 AA;  
SQ  
Query Match 92.0%; Score 332; DB 21; Length 70;  
Best Local Similarity 92.9%; Pred. No. 1e-35;  
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEALQIIAAIPEKYLQFHNLSNL 60  
DB 1 TLVWGEAAVDGSRGCGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70  
RESULT 9  
AAB18678  
ID AAB18678 standard; peptide; 70 AA.  
XX  
AC AAB18678;  
XX  
XX 22-JAN-2001 (first entry)  
XX  
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
KW ribosome binding region; resistance; geminivirus infection.  
XX  
OS Synthetic.  
OS Tomato golden mosaic virus.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 12 /note= "wild type residue replaced with Ala"  
FT FT Misc-difference 13 /note= "wild type residue replaced with Ala"  
FT FT Misc-difference 15 /note= "wild type residue replaced with Ala"  
XX  
XX WO200054573-A1.  
XX  
XX 21-SEP-2000.  
XX  
XX 15-MAR-2000; 2000WO-US06759.  
XX  
XX 18-MAR-1999; 99US-0125004.  
XX 09-APR-1999; 99US-0289346.  
XX  
XX (UYNC-) UNIV NORTH CAROLINA STATE.  
XX

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XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT Transgenic plants with increased resistance to geminivirus infection
XX FT comprise a nucleic acid construct containing a nucleic acid sequence
XX FT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PS Claim 53; Page 42-43; 73pp; English.
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 91.7%; Score 331; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.3e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEALQIIAAAIPEKYLQFHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEALQIIAAAIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 10
AAB18686
ID AAB18686 standard; peptide; 70 AA.
AC AAB18686;
DT 22-JAN-2001 (first entry)
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
OS Synthetic.
XX OS Tomato golden mosaic virus.
XX FH Key Location/Qualifiers
FT Misc-difference 24 /note= "wild type residue replaced with Leu"
FT Misc-difference 25 /note= "wild type residue replaced with Leu"
FT Misc-difference 26 /note= "wild type residue replaced with Leu"
XX FT Misc-difference 26 /note= "wild type residue replaced with Leu"
XX FN WO200054573-A1.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000; 2000WO-US06759.
XX PR 18-MAR-1999; 99US-0125004.

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PR 09-APR-1999; 99US-0289346.
XX (UTNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT Transgenic plants with increased resistance to geminivirus infection
XX FT comprise a nucleic acid construct containing a nucleic acid sequence
XX FT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PS Claim 53; Page 46; 73pp; English.
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 91.7%; Score 331; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.3e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEALQIIAAAIPEKYLQFHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTNDLLLEALNASSKEALQIIREKIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 11
AAB18689
ID AAB18689 standard; peptide; 70 AA.
AC AAB18689;
DT 22-JAN-2001 (first entry)
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
OS Synthetic.
XX OS Tomato golden mosaic virus.
XX FH Key Location/Qualifiers
FT Misc-difference 22 /note= "wild type residue replaced with Ala"
FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX FN WO200054573-A1.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000; 2000WO-US06759.
XX PR

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PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant ALI protein with a mutation in the Rb binding region
XX
XX Disclosure; Page 48-49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as ALI. ALI binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the ALI
XX protein are used to produce transgenic plants. The mutation in ALI is
XX present in a ribosome binding region, and expression of mutant ALI
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant ALI proteins are useful for producing plants having
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 91.4%; Score 330; DB 21; Length 70;
XX Best Local Similarity 92.9%; Pred. No. 1.8e-35;
XX Matches 55; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEALQIIAAAIPEKYLQFHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEALQIIAAAIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
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RESULT 12
AAB18691
ID AAB18691 standard; peptide; 70 AA.
XX
XX AAB18691;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (ALI) protein.
XX
XX Geminivirus; replication protein; Rep protein; ALI; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 34 /note= "wild type residue replaced with Ala"
XX Misc-difference 35 /note= "wild type residue replaced with Ala"
XX Misc-difference 36 /note= "wild type residue replaced with Ala"
XX WO200054573-A1.
XX
XX 21-SEP-2000.
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XX 15-MAR-2000; 2000WO-US06759.
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XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant ALI protein with a mutation in the Rb binding region
XX
XX Disclosure; Page 49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as ALI. ALI binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the ALI
XX protein are used to produce transgenic plants. The mutation in ALI is
XX present in a ribosome binding region, and expression of mutant ALI
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant ALI proteins are useful for producing plants having
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 90.9%; Score 328; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 3.3e-35;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
QY 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEALQIIAAAIPEKYLQFHNLSNL 60
DB 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEALQIIAAAIPEKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
XX
RESULT 13
AAB18681
ID AAB18681 standard; peptide; 70 AA.
XX
XX AAB18681;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (ALI) protein.
XX
XX Geminivirus; replication protein; Rep protein; ALI; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 47 /note= "wild type residue replaced with Ala"
XX Misc-difference 48 /note= "wild type residue replaced with Ala"
XX Misc-difference 49 /note= "wild type residue replaced with Ala"
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX

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PN W0200054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPT; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Claim 52; Page 44; 73pp; English.  
 XX The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, bean dwarf mosaic virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX Sequence 70 AA;  
 SQ Query Match 90.0%; Score 325; DB 21; Length 70;  
 Best Local Similarity 91.4%; Pred. No. 8.3e-35;  
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 TLVWGEFQVGRSARGCGQTSNDAAALNASSKEALQIIAAAIPEKYLQFPHNLNSNL 60  
 Db 1 TLVWGEFQVGRSARGCGQTSNDAAALNASSKEALQIIREKIPAAALFQPHNLNSNL 60  
 Qy 61 DRIFDKTPEP 70  
 Db 61 DRIFDKTPEP 70  
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 AAB18683  
 ID AAB18683 standard; peptide; 70 AA.  
 AC AAB18683;  
 XX 22-JAN-2001 (first entry)  
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.  
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX Key Location/Qualifiers  
 FT Misc-difference 59 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 61 /note= "wild type residue replaced with Ala"

FT Misc-difference 62 /note= "wild type residue replaced with Ala"  
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 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPT; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Claim 53; Page 45; 73pp; English.  
 XX The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, bean dwarf mosaic virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX Sequence 70 AA;  
 SQ Query Match 89.8%; Score 324; DB 21; Length 70;  
 Best Local Similarity 91.4%; Pred. No. 1.1e-34;  
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 TLVWGEFQVGRSARGCGQTSNDAAALNASSKEALQIIAAAIPEKYLQFPHNLNSNL 60  
 Db 1 TLVWGEFQVGRSARGCGQTSNDAAALNASSKEALQIIREKIPKYLQFPHNLNSAL 60  
 Qy 61 DRIFDKTPEP 70  
 Db 61 AAFDKTPEP 70  
 RESULT 15  
 AAB18682  
 ID AAB18682 standard; peptide; 70 AA.  
 AC AAB18682;  
 XX 22-JAN-2001 (first entry)  
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.  
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX Key Location/Qualifiers  
 FT Misc-difference 52

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FT      /note= "wild type residue replaced with Ala"
FT Misc-difference 54
FT      /note= "wild type residue replaced with Ala"
FT Misc-difference 55
FT      /note= "wild type residue replaced with Ala"
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XX WO200054573-A1.
XX
XX PD 21-SEP-2000.
XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX
XX PR 18-MAR-1999; 99US-0125004.
XX
XX PR 09-APR-1999; 99US-0289346.
XX
XX (UYN-) UNIV NORTH CAROLINA STATE.
XX
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WP1; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 53; Page 44-45; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX SQ Sequence 70 AA;
XX
XX Query Match 89.2%; Score 322; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 2e-34;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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XX QY 1 TLVWGEFQVDSARGCCTNSDAAAEALNASSKEEALQITAAATPEKYLFEHNLNSNL 60
XX   |||||||
XX Db 1 TLVWGEFQVDSARGCCTNSDAAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
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XX QY 61 DRIFDKTPEP 70
XX   |||||||
XX Db 61 DRIFDKTPEP 70

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 Job time : 32.6667 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 11.6667 Seconds  
(without alignments)  
253.865 Million cell updates/sec

Title: US-09-289-346B-4

Perfect score: 361

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	219	60.7	353	3	US-08-838-151A-44
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7	219	60.7	353	3	US-08-838-151A-49
8	219	60.7	353	3	US-08-838-151A-52
9	219	60.7	353	3	US-08-838-151A-55
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16	200	55.4	357	3	US-08-838-151A-30
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20	60.5	16.8	131	3	US-08-838-151A-14
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23	58.5	16.2	356	1	US-08-781-582-1
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38 54.5 15.1 1713 5 PCT-US94-10261A-24  
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#### ALIGNMENTS

#### RESULT 1

US-08-809-103B-2

; Sequence 2, Application US/08809103B

; Patent No. 6133505

; GENERAL INFORMATION:

; APPLICANT: GROENBORN, Bruno

; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSER: YOUNG & THOMPSON

; STREET: 745 South 23rd Street

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/809,103B

; FILING DATE: 17-MAR-1997

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PR 94.11040

; FILING DATE: 15-SEP-1994

; APPLICATION NUMBER: WO PCT/FR95/01192

; FILING DATE: 15-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: PATCH, Andrew J.

; REGISTRATION NUMBER: 32,925

; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 521-2297

; TELEFAX: (703) 685-0573

; TELEX: 248425 EMBON

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 359 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-809-103B-2

Query Match 61.5%; Score 222; DB 3; Length 359;

Best Local Similarity 58.0%; Pred. No. 5,3e-22;

Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

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Db 111 LEWGTFTQIDGSRAGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSLD 170  
Qy 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

RESULT 2  
US-08-809-103B-4  
; Sequence 4, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994

; PRIOR APPLICATION NUMBER: WO PCT/FR95/01192  
; FILING DATE: 15-SEP-1995  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-809-103B-4  
Query Match 61.5%; Score 222; DB 3; Length 359;  
Best Local Similarity 59.0%; Pred. No. 5.3e-22;  
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;  
Qy 2 LVWGFEVDGSRAGGCGQTNDAAAEALNASSKEEALQIIIAAIPKYLQFPHNLNSLD 61  
Db 111 LEWGTFTQIDGSRAGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSLD 170  
Qy 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

RESULT 3  
US-08-809-103B-6  
; Sequence 6, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; PRIOR APPLICATION NUMBER: WO PCT/FR95/01192  
; FILING DATE: 15-SEP-1995  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-809-103B-4  
Query Match 61.5%; Score 222; DB 3; Length 359;  
Best Local Similarity 59.0%; Pred. No. 5.3e-22;  
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;  
Qy 2 LVWGFEVDGSRAGGCGQTNDAAAEALNASSKEEALQIIIAAIPKYLQFPHNLNSLD 61  
Db 111 LEWGTFTQIDGSRAGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSLD 170  
Qy 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

RESULT 4  
US-08-809-103B-8  
; Sequence 8, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; PRIOR APPLICATION NUMBER: WO PCT/FR95/01192  
; FILING DATE: 15-SEP-1995  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-809-103B-6  
Query Match 61.5%; Score 222; DB 3; Length 359;  
Best Local Similarity 58.0%; Pred. No. 5.3e-22;  
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;  
Qy 2 LVWGFEVDGSRAGGCGQTNDAAAEALNASSKEEALQIIIAAIPKYLQFPHNLNSLD 61  
Db 111 LEWGTFTQIDGSRAGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSLD 170  
Qy 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

RESULT 4  
US-08-809-103B-8  
; Sequence 8, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; PRIOR APPLICATION NUMBER: WO PCT/FR95/01192  
; FILING DATE: 15-SEP-1995  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-809-103B-6  
Query Match 61.5%; Score 222; DB 3; Length 359;  
Best Local Similarity 58.0%; Pred. No. 5.3e-22;  
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;  
Qy 2 LVWGFEVDGSRAGGCGQTNDAAAEALNASSKEEALQIIIAAIPKYLQFPHNLNSLD 61  
Db 111 LEWGTFTQIDGSRAGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSLD 170  
Qy 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

RESULT 4  
US-08-809-103B-8  
; Sequence 8, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; PRIOR APPLICATION NUMBER: WO PCT/FR95/01192  
; FILING DATE: 15-SEP-1995  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-809-103B-6  
Query Match 61.5%; Score 222; DB 3; Length 359;  
Best Local Similarity 58.0%; Pred. No. 5.3e-22;  
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;  
Qy 2 LVWGFEVDGSRAGGCGQTNDAAAEALNASSKEEALQIIIAAIPKYLQFPHNLNSLD 61  
Db 111 LEWGTFTQIDGSRAGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSLD 170  
Qy 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

RESULT 4  
US-08-809-103B-8  
; Sequence 8, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; PRIOR APPLICATION NUMBER: WO PCT/FR95/01192  
; FILING DATE: 15-SEP-1995  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-809-103B-6  
Query Match 61.5%; Score 222; DB 3; Length 359;  
Best Local Similarity 58.0%; Pred. No. 5.3e-22;  
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;  
Qy 2 LVWGFEVDGSRAGGCGQTNDAAAEALNASSKEEALQIIIAAIPKYLQFPHNLNSLD 61  
Db 111 LEWGTFTQIDGSRAGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSLD 170  
Qy 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: US94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8

Query Match 61.5%; Score 222; DB 3; Length 359;
Best Local Similarity 58.0%; Pred. No. 5.3e-22;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDRGARGGQTSNDAAAEALNASSKEALQIIAAAIPEKYLQFHNLSNLD 61
Db 111 LWTGFIQDRGARGGQTSNDAAAEALNASSKEALQIIAAAIPEKYLQFHNLSNLD 170
QY 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 5
US-08-838-151A-44
; Sequence 44, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

Query Match 60.7%; Score 219; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 1.3e-21;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-44

Query Match 60.7%; Score 219; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 1.3e-21;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLWGEFQVDRGARGGQTSNDAAAEALNASSKEALQIIAAAIPEKYLQFHNLSNLD 60
Db 110 TIWGEFQVDRGARGGQTSNDAAAEALNASSKEALQIIAAAIPEKYLQFHNLSNLD 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 6
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

Query Match 60.7%; Score 219; DB 3; Length 353;

```





QY 61 DRIFDKTPEP 70  
 :|||:|  
 Db 170 ERIFAKAPEP 179

## RESULT 12

US-08-838-151A-6  
 ; Sequence 6, Application US/08838151A  
 ; Patent No. 6291743  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stout, John T  
 ; APPLICANT: Luu, Hang T  
 ; APPLICANT: Maxwell, Douglas  
 ; APPLICANT: Ahlquist, Paul  
 ; APPLICANT: Hanson, Steve  
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
 ; NUMBER OF SEQUENCES: 63  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
 ; STREET: Two Prudential Plaza, Suite 4700  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: U.S.A.  
 ; ZIP: 60601  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/838,151A  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mueller, Lisa V  
 ; REGISTRATION NUMBER: 38,978  
 ; REFERENCE/DOCKET NUMBER: SVS3801P0260  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-616-5400  
 ; TELEFAX: 312-616-5460  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 361 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-838-151A-6

Query Match 59.3%; Score 214; DB 3; Length 361;  
 Best Local Similarity 55.7%; Pred. No. 6.6e-21;  
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDRSARGGCGTSDNDAABALNASSKEALQITAAIPEKYLQFHNLSNL 60  
 :|||:|  
 Db 110 TIEWGDFQIDGRSARGGQGSANDSYAKALNASSVQSALAVLRREQPKDFVLQNHNSNL 169  
 :|||:|  
 QY 61 DRIFDKTPEP 70  
 :|||:|  
 Db 170 ERIFAKAPEP 179

US-08-838-151A-6  
 ; Sequence 6, Application US/08838151A  
 ; Patent No. 6291743  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stout, John T  
 ; APPLICANT: Luu, Hang T  
 ; APPLICANT: Maxwell, Douglas  
 ; APPLICANT: Ahlquist, Paul  
 ; APPLICANT: Hanson, Steve  
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
 ; NUMBER OF SEQUENCES: 63  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
 ; STREET: Two Prudential Plaza, Suite 4700  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: U.S.A.  
 ; ZIP: 60601  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/838,151A  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mueller, Lisa V  
 ; REGISTRATION NUMBER: 38,978  
 ; REFERENCE/DOCKET NUMBER: SVS3801P0260  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-616-5400  
 ; TELEFAX: 312-616-5460  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 361 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-838-151A-6

Query Match 59.3%; Score 214; DB 3; Length 361;  
 Best Local Similarity 55.7%; Pred. No. 6.6e-21;  
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDRSARGGCGTSDNDAABALNASSKEALQITAAIPEKYLQFHNLSNL 60  
 :|||:|  
 Db 110 TIEWGDFQIDGRSARGGQGSANDSYAKALNASSVQSALAVLRREQPKDFVLQNHNSNL 169  
 :|||:|  
 QY 61 DRIFDKTPEP 70  
 :|||:|  
 Db 170 ERIFAKAPEP 179

## RESULT 13

US-08-838-151A-8  
 ; Sequence 8, Application US/08838151A  
 ; Patent No. 6291743  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stout, John T  
 ; APPLICANT: Luu, Hang T  
 ; APPLICANT: Maxwell, Douglas  
 ; APPLICANT: Ahlquist, Paul  
 ; APPLICANT: Hanson, Steve  
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus

; TITLE OF INVENTION: Genes  
 ; NUMBER OF SEQUENCES: 63  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
 ; STREET: Two Prudential Plaza, Suite 4700  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: U.S.A.  
 ; ZIP: 60601  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/838,151A  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mueller, Lisa V  
 ; REGISTRATION NUMBER: 38,978  
 ; REFERENCE/DOCKET NUMBER: SVS3801P0260  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-616-5400  
 ; TELEFAX: 312-616-5460  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 361 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-838-151A-8

Query Match 59.3%; Score 214; DB 3; Length 361;  
 Best Local Similarity 55.7%; Pred. No. 6.6e-21;  
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDRSARGGCGTSDNDAABALNASSKEALQITAAIPEKYLQFHNLSNL 60  
 :|||:|  
 Db 110 TIEWGDFQIDGRSARGGQGSANDSYAKALNASSVQSALAVLRREQPKDFVLQNHNSNL 169  
 :|||:|  
 QY 61 DRIFDKTPEP 70  
 :|||:|  
 Db 170 ERIFAKAPEP 179

## RESULT 14

US-08-838-151A-24  
 ; Sequence 24, Application US/08838151A  
 ; Patent No. 6291743  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stout, John T  
 ; APPLICANT: Luu, Hang T  
 ; APPLICANT: Maxwell, Douglas  
 ; APPLICANT: Ahlquist, Paul  
 ; APPLICANT: Hanson, Steve  
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
 ; NUMBER OF SEQUENCES: 63  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
 ; STREET: Two Prudential Plaza, Suite 4700  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: U.S.A.  
 ; ZIP: 60601  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/838,151A

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;
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-24

Query Match      55.4%; Score 200; DB 3; Length 357;
Best Local Similarity 63.9%; Pred. No. 5.3e-19;
Matches 39; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY      4 WGEFQVDGRSARGGCQTSNDAAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSNLDRI 63
Db      111 FGVSIQDGRSARGGQSQSANDAYAEALNSGSKSEALNLIKKEAPKDYILQFHNLSNLDRI 170

QY      64 F 64
Db      171 F 171

RESULT 15
US-08-838-151A-27
; Sequence 27, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminitivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS: 63
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-27
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Query Match      55.4%; Score 200; DB 3; Length 357;
Best Local Similarity 63.9%; Pred. No. 5.3e-19;
Matches 39; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY      4 WGEFQVDGRSARGGCQTSNDAAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSNLDRI 63
Db      111 FGVSIQDGRSARGGQSQSANDAYAEALNSGSKSEALNLIKKEAPKDYILQFHNLSNLDRI 170

QY      64 F 64
Db      171 F 171

Search completed: December 23, 2003, 08:59:33
Job time : 11.6667 secs
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds  
(without alignments)  
172.015 Million cell updates/sec

Title: US-09-289-346B-4  
Perfect score: 361  
Sequence: 1 TLVWGEFQVDSRGSGCQT.....FQFHNLNLDRIFDKTEP 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

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Database : Published Applications AA:\*

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- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_PUB.pdb\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pdb\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pdb\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pdb\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB\_PUB.pdb\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pdb\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pdb\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pdb\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB\_PUB.pdb\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB\_PUB.pdb\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pdb\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361	100.0	70	10	US-09-289-346A-4
2	346	95.8	70	10	US-09-289-346A-1
3	346	95.8	356	10	US-09-289-346A-11
4	338	93.6	70	10	US-09-289-346A-9
5	335	92.8	70	10	US-09-289-346A-12
6	334	92.5	70	10	US-09-289-346A-16
7	332	92.0	70	10	US-09-289-346A-8
8	332	92.0	70	10	US-09-289-346A-14
9	331	91.7	70	10	US-09-289-346A-2
10	331	91.7	70	10	US-09-289-346A-10
11	330	91.4	70	10	US-09-289-346A-13
12	328	90.9	70	10	US-09-289-346A-15
13	325	90.0	70	10	US-09-289-346A-5
14	324	89.8	70	10	US-09-289-346A-7
15	322	89.2	70	10	US-09-289-346A-6

16	314	87.0	70	10	US-09-289-346A-3	Sequence 3, Appli
17	65.5	18.1	512	12	US-10-301-661A-4	Sequence 4, Appli
18	61.5	17.0	1217	15	US-10-156-761-13942	Sequence 13942, A
19	61	16.9	483	10	US-09-738-626-5097	Sequence 5097, Ap
20	60	16.6	821	12	US-10-032-585-7131	Sequence 7131, Ap
21	59	16.3	1502	10	US-09-801-368-140	Sequence 140, App
22	58.5	16.2	356	10	US-09-898-216-1	Sequence 1, Appli
23	58.5	16.2	590	10	US-09-934-060A-13	Sequence 13, Appli
24	58.5	16.2	720	10	US-09-934-060A-2	Sequence 2, Appli
25	58.5	16.2	720	10	US-09-934-060A-4	Sequence 4, Appli
26	58.5	16.2	3007	12	US-10-291-172-222	Sequence 222, App
27	58	16.1	272	9	US-09-804-969-19	Sequence 19, Appli
28	58	16.1	340	10	US-09-835-996A-19	Sequence 19, Appli
29	58	16.1	340	12	US-10-094-749-2976	Sequence 2976, Ap
30	58	16.1	567	10	US-09-835-996A-8	Sequence 8, Appli
31	58	16.1	588	15	US-10-128-714-8568	Sequence 8568, Ap
32	58	16.1	596	15	US-10-128-714-3568	Sequence 3568, Ap
33	58	16.1	759	15	US-10-258-860-6	Sequence 6, Appli
34	58	16.1	762	10	US-09-804-969-15	Sequence 15, Appli
35	58	16.1	762	10	US-09-808-664-2	Sequence 2, Appli
36	58	16.1	785	15	US-10-258-860-2	Sequence 2, Appli
37	58	16.1	785	15	US-10-258-860-4	Sequence 4, Appli
38	57.5	15.9	304	12	US-09-882-227-590	Sequence 590, App
39	57	15.8	211	15	US-10-156-761-10576	Sequence 10576, A
40	57	15.8	603	12	US-10-071-362-27	Sequence 27, Appli
41	57	15.8	836	11	US-09-972-708-9	Sequence 9, Appli
42	56	15.5	233	12	US-09-949-029-8	Sequence 8, Appli
43	56	15.5	367	11	US-09-932-367A-20	Sequence 20, Appli
44	55.5	15.4	299	8	US-08-831-310-2	Sequence 2, Appli
45	55.5	15.4	299	10	US-09-881-752A-244	Sequence 244, App

## ALIGNMENTS

## RESULT 1

US-09-289-346A-4  
; Sequence 4, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orosco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Grullem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (42)..(44)  
; OTHER INFORMATION: Description of Artificial sequence: Fragment of  
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine  
; OTHER INFORMATION: replacements (REK154->AAA154).  
US-09-289-346A-4

Query Match 100.0%; Score 361; DB 10; Length 70;  
Best Local Similarity 100.0%; Pred. No. 1e-40;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGCQTNDAAAEALNASSKEALQIIAAAIPEKYLQFPHNLNSL 60  
Db 1 TLVWGEFQVDSRGSGCQTNDAAAEALNASSKEALQIIAAAIPEKYLQFPHNLNSL 60  
QY 61 DRIFDKTEP 70



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Db          61 DRIFDKTPEP 70
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110 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 169

RESULT 2
US-09-289-346A-1
; Sequence 1, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-1

Query Match          95.8%; Score 346; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 1e-38; 3; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 0;

QY 1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIAAIPEKYLFOFHNLSNL 60
|||||
Db 1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
|||||
Db 61 DRIFDKTPEP 70

RESULT 3
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11

Query Match          95.8%; Score 346; DB 10; Length 356;
Best Local Similarity 95.7%; Pred. No. 8.9e-38; 3; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 0;

QY 1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIAAIPEKYLFOFHNLSNL 60
|||||

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Db          61 DRIFDKTPEP 70
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110 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 169

RESULT 4
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9

Query Match          93.6%; Score 338; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 1.2e-37; 4; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 4;

QY 1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIAAIPEKYLFOFHNLSNL 60
|||||
Db 1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
|||||
Db 61 DRIFDKTPEP 70

RESULT 5
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12

Query Match          92.8%; Score 335; DB 10; Length 70;

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```
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->AAl18) .
US-09-289-346A-8

Query Match          92.0%; Score 332; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 7.7e-37;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIAAAIPEKYLQFPHNLNSNL 60
   |||||
Db 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 6
US-09-289-346A-16
; Sequence 16, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-(9-289-346A-16

Query Match          92.5%; Score 334; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 4.1e-37;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIAAAIPEKYLQFPHNLNSNL 60
   |||||
Db 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
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QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 7
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)..(8)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
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```
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->AAl18) .
US-09-289-346A-8

Query Match          92.0%; Score 332; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 7.7e-37;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIAAAIPEKYLQFPHNLNSNL 60
   |||||
Db 1 TLVWGEAAVDGSRAGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 8
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14

Query Match          92.0%; Score 332; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 7.7e-37;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIAAAIPEKYLQFPHNLNSNL 60
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Db 1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 9
US-09-289-346A-2
; Sequence 2, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
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; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
; US-09-289-346A-2

Query Match          91.7%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1e-36;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIAAAIPEKYLQFHNLSNL 60
DB 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; US-09-289-346A-10

Query Match          91.7%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1e-36;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIAAAIPEKYLQFHNLSNL 60
DB 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; US-09-289-346A-13

Query Match          91.7%; Score 331; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1e-36;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIAAAIPEKYLQFHNLSNL 60
DB 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; US-09-289-346A-15

Query Match          90.9%; Score 328; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 2.6e-36;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIAAAIPEKYLQFHNLSNL 60
DB 1 TLVWGFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS

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; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (EKY159->AAA159).
US-09-289-346A-5

Query Match      90.0%; Score 325; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 6.7e-36;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLSNL 60
   |||||
Db 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPAAALFOFHNLSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 14
US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (59)..(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDRI172->ALAA172).
US-09-289-346A-7

Query Match      89.8%; Score 324; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 9.1e-36;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLSNL 60
   |||||
Db 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYLFOFHNLSAL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 AAIFDKTPEP 70
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RESULT 15
US-09-289-346A-6
; Sequence 6, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (52)..(55)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (QFHN165->AFAA165).
US-09-289-346A-6

Query Match      89.2%; Score 322; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.7e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLSNL 60
   |||||
Db 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

Search completed: December 23, 2003, 09:43:29
Job time : 76 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds  
(without alignments)  
673.181 Million cell updates/sec

Title: US-09-289-346B-4  
Perfect score: 361  
Sequence: 1 TLVWGEFQVDSARGGCGT.....PQFHNLSNLDRIFDKTPPEP 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*  
1: Pir1:\*  
2: Pir2:\*  
3: Pir3:\*  
4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	346	95.8	352	1 QOCVLI	AL1 protein - toma
2	249	69.0	361	1 QOCVPT	AL1 protein - pota
3	240	66.5	358	2 S07594	hypothetical prote
4	233	64.5	362	1 J01887	AL1 protein - toma
5	229	63.4	359	2 S39211	gene C1 protein -
6	222	61.5	349	2 J02300	replicase - pepper
7	222	61.5	349	2 S31875	AL1 protein - pepp
8	222	61.5	359	2 S22593	hypothetical prote
9	219	60.7	359	2 S39235	gene C1 protein -
10	216	59.8	351	2 J02327	AL1 protein - Indi
11	216	59.8	355	1 QOCVM1	AV1 protein - abut
12	213	59.0	385	2 S28360	AL1 protein - beet
13	210	58.2	358	1 J01870	AL1 protein - toma
14	200	55.4	357	1 QOCVC1	AL1 protein - toma
15	199	55.1	360	2 S59885	replication-associ
16	134	37.1	131	2 S45059	AC1 protein (clone
17	128	35.5	347	1 QOCVS1	AL1 protein - squa
18	72	19.9	587	2 J01419	Fc gamma (IgG) rec
19	68	18.8	714	2 C95382	probable ferrichro
20	63.5	17.6	584	2 T19061	hypothetical prote
21	62.5	17.3	1006	2 S74992	hypothetical prote
22	61.5	17.0	299	2 B71967	probable peptidyl-
23	61.5	17.0	335	1 DBBSGF	glyceraldehyde-3-p
24	61.5	17.0	481	2 A70091	probable phosphoe
25	61.5	17.0	1044	2 T43800	protein kinase bub
26	61.5	17.0	1203	2 T17415	mycelial surface a
27	61.5	17.0	1229	2 T48959	kinesin-like prote
28	60.5	16.8	159	2 C71838	NADH2 dehydrogenas
29	60.5	16.8	159	2 E64677	NADH2 dehydrogenas

30	60.5	16.8	819	2	AI3197	TonB-dependent rec
31	60	16.6	767	2	F71479	hypothetical prote
32	60	16.6	1008	2	T41244	SEC14 protein homo
33	59	16.3	160	2	G82060	hypothetical prote
34	59	16.3	201	2	AE2732	NADH ubiquinone ox
35	59	16.3	201	2	G97513	NADH dehydrogenase
36	59	16.3	228	2	F90130	hypothetical prote
37	59	16.3	338	2	AG3582	iron(III)-binding
38	59	16.3	1502	1	RGBYH1	CYC1/CYP3 transcr
39	58.5	16.2	297	1	MNVNRV	nonstructural prot
40	58.5	16.2	357	2	T02246	protein C17D12-7
41	58.5	16.2	569	2	H87926	hypothetical prote
42	58.5	16.2	642	2	D90558	topoisomerase iv s
43	58.5	16.2	769	2	F81742	conserved hypothet
44	58.5	16.2	2135	2	T14602	variant-specific s
45	58	16.1	345	2	AD3024	hypothetical prote

ALIGNMENTS

RESULT 1

QOCVLI  
AL1 protein - tomato golden mosaic virus  
C:Species: tomato golden mosaic virus  
A:Note: host Nicotiana sp. (tobacco)  
C>Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Apr-1994  
C:Accession: A04170  
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.  
EMBO J. 3, 2197-2205, 1984  
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat  
A:Reference number: A04163  
A:Accession: A04170  
A:Molecule type: DNA  
A:Residues: 1-352 <HAM>  
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match	95.8%	Score	346;	DB	1;	Length	352;
Best Local Similarity	95.7%	Pred. No.	4.2e-33;	Mismatches	3;	Indels	0;
Matches	67;	Conservative	0;	0;	Gaps	0;	0;
QY	1	TLVWGEFQVDSARGGCGTGNDAALNASSKEALQIIAAAIPEKYLFOFHNLSNL	60				
Db	111	TLVWGEFQVDSARGGCGTGNDAALNASSKEALQIIREKIPEKYLFOFHNLSNL	170				
QY	61	DRIFDKTPPEP	70				
Db	171	DRIFDKTPPEP	180				

RESULT 2

QOCVPT  
AL1 protein - potato yellow mosaic virus (isolate Venezuela)  
C:Species: potato yellow mosaic virus  
C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jun-2000  
C:Accession: J00364  
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.  
J. Gen. Virol. 72, 1515-1520, 1991  
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel  
A:Reference number: J00362; MUID:91311403; PMID:1856690  
A:Accession: J00364  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-361 <COU>  
A:Cross-references: GB:D00940; NID:g222458; PIDN:BAA00782.1; PID:g222459  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 69.0%; Score 249; DB 1; Length 361;  
Best Local Similarity 68.1%; Pred. No. 1.3e-21;  
Matches 47; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGCQTSNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNL 60  
DB 110 TLVWGLFQIDGSRGCGQTVNDAAAEALNSGTEAKMKIIEKPEKFLQYHNLSCNL 169

QY 61 DRIFDKTPE 69  
DB 170 DRIFDKAPE 178

RESULT 3  
S07594  
hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)  
C/Species: cassava latent virus  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Sep-1999  
C/Accession: S07594  
R/Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.  
Nucleic Acids Res. 18, 197-198, 1990  
A/Title: Nucleotide sequence of the infectious cloned DNA components of African cassava  
A/Reference number: S07590; MUID:90174930; PMID:2308831  
A/Accession: S07594  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-358 <MOR>  
A/Cross-references: EMBL:X17095; NID:G59371; PIDN:CAA34953.1; PID:G59376  
C/Genetics:  
A/Map position: segment DNAL  
C/Superfamily: tomato golden mosaic virus ALL protein

Query Match 66.5%; Score 240; DB 2; Length 358;  
Best Local Similarity 61.4%; Pred. No. 1.5e-20;  
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGCQTSNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNL 60  
DB 109 TVWGEFQIDGSRGCGQTSNDAAAEALNASGSKSEALNRELVPKDFLOFHNLSNL 168

QY 61 DRIFDKTPE 70  
DB 169 DRIFQEPAP 178

RESULT 4  
JQ1887  
ALL protein - tomato yellow leaf curl virus (strain Australia)  
N/Alternate names: CI protein  
C/Species: tomato yellow leaf curl virus  
C/Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 07-May-1999  
C/Accession: JQ1887  
R/Dry, I.B.; Rigden, J.E.; Krake, L.R.; Mullineaux, P.M.; Rezaian, M.A.  
J. Gen. Virol. 74, 147-151, 1993  
A/Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.  
A/Reference number: JQ1885; MUID:93139778; PMID:8423446  
A/Accession: JQ1887  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-362 <DRY>  
A/Cross-references: GB:S53251  
C/Superfamily: tomato golden mosaic virus ALL protein

Query Match 64.5%; Score 233; DB 1; Length 362;  
Best Local Similarity 54.1%; Pred. No. 1e-19;  
Matches 46; Conservative 9; Mismatches 14; Indels 16; Gaps 1;

QY 1 TLVWGEFQVDSARGCGCQTSNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNL 60  
DB 110 TLEWGEFQIDGSRGCGQTSNDAAAEALNLTGSKSEALNRELAPKDYVLQFHNLSNL 169

QY 61 DRI-----FDKTP 69  
|||

DB 170 DRIFPPLEVYVSPFLSSSFDVRPE 194

RESULT 5  
S39211  
gene CI protein - tomato yellow leaf curl virus  
C/Species: tomato yellow leaf curl virus  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Sep-1999  
C/Accession: S39211  
R/Noris, E.; Hidalgo, E.; Accotto, G.; Moriones, B.  
submitted to the EMBL Data Library, August 1993  
A/Description: High similarity among the tomato yellow leaf curl virus isolates from th  
A/Reference number: S39209  
A/Accession: S39211  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-359 <NOR>  
A/Cross-references: EMBL:Z25751; NID:G433655; PIDN:CAA81026.1; PID:G433658  
C/Superfamily: tomato golden mosaic virus ALL protein

Query Match 63.4%; Score 229; DB 2; Length 359;  
Best Local Similarity 60.9%; Pred. No. 3e-19;  
Matches 42; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDSARGCGCQTSNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNL 61  
DB 111 LEMGTQIDGSRGCGQTSNDAAAEALNAGSKSEALDIKELAPRDYILHFNINSNL 170

QY 62 RIFDKTPEP 70  
DB 171 RVFQVPPAP 179

RESULT 6  
JQ2300  
replicase - pepper huasteco virus (component A)  
N/Alternate names: ORF ALL protein  
C/Species: pepper huasteco virus  
C/Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 20-Sep-1999  
C/Accession: JQ2300  
R/Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Herrera-Estrella, L.; Rivera-Bustamante, R.  
J. Gen. Virol. 74, 2225-2231, 1993  
A/Title: Complete nucleotide of pepper huasteco virus: Analysis and comparison with b  
A/Reference number: JQ2299; MUID:94015007; PMID:8409944  
A/Accession: JQ2300  
A/Molecule type: DNA  
A/Residues: 1-349 <TOR>  
A/Cross-references: GB:X70418; NID:G61023; PIDN:CAA49856.1; PID:G61025  
C/Superfamily: tomato golden mosaic virus ALL protein

Query Match 61.5%; Score 222; DB 2; Length 349;  
Best Local Similarity 60.0%; Pred. No. 1.9e-18;  
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGCQTSNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNL 60  
DB 110 TVWGEFQIDGSRGCGQTSNDAAAEALNAGSKSEALDIKELAPRDYILHFNINSNL 169

QY 61 DRIFDKTPEP 70  
DB 170 NRIFQTPPEP 179

RESULT 7  
S31875  
ALL protein - pepper rizado amarillo virus  
C/Species: pepper rizado amarillo virus  
C/Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 20-Sep-1999  
C/Accession: S31875  
R/Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera-I  
submitted to the EMBL Data Library, February 1993  
A/Description: Complete nucleotide sequence of pepper huasteco virus: analysis and com  
A/Reference number: S31872

A:Accession: S31875  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <TOR>  
A:Cross-references: EMBL:X70418; NID:G61023; PIDN:CAA49856.1; PID:G61025  
A>Note: the source is designated as pepper huasteco virus  
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 61.5%; Score 222; DB 2; Length 349;

Best Local Similarity 60.0%; Pred. No. 1.9e-18;

Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGCGCQTSNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNL 60  
DB 110 TVWGEFQIDGRSARGGQQTANDAYAKAINAGSKSEALDIKQLAPRDYVLFHFHNSNLD 169

QY 61 DRIFDKTPEP 70

DB 170 NRIFQTPPEP 179

#### RESULT 8

S22593

hypothetical protein C4 - tomato yellow leaf curl virus

C:Species: tomato yellow leaf curl virus

C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Sep-1999

C:Accession: S22593

R:Kheyr-Pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.

Nucleic Acids Res. 19, 6763-6769, 1991

A:Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite

A:Reference number: S22588; MUID:92107660; PMID:1840676

A:Accession: S22593

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-359 <KHE>

A:Cross-references: EMBL:X61153; NID:G62211; PIDN:CAA43466.1; PID:G62217

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 61.5%; Score 222; DB 2; Length 359;

Best Local Similarity 58.0%; Pred. No. 2e-18;

Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGFQVDSARGCGCQTSNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNLD 61

DB 111 LEWGFQIDGRSARGGQQTANDAYAKAINAGSKSEALDIKQLAPRDYVLFHFHNSNLD 170

QY 62 RIFDKTPEP 70

DB 171 KVQVPPAP 179

#### RESULT 9

S39235

gene C1 protein - tomato yellow leaf curl virus

C:Species: tomato yellow leaf curl virus

C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Sep-1997

C:Accession: S39235

R:Crespi, S.; Noris, E.; Vaira, A.; Bosco, D.; Accotto, G.

submitted to the EMBL Data Library, December 1993

A:Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.

A:Reference number: S39233

A:Accession: S39235

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-359 <CRE>

A:Cross-references: EMBL:Z28390; NID:G1041671; PID:G1334964

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match

Best Local Similarity 60.7%; Score 219; DB 2; Length 359;

Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGFQVDSARGCGCQTSNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNLD 61  
DB 111 LEWGFQIDGRSARGGQQTANDAYAKAINAGSKSEALDIKQLAPRDYVLFHFHNSNLD 170

QY 62 RIFDKTPEP 70

DB 171 KVQVPPAP 179

#### RESULT 10

QY2327

ALI protein - Indian cassava mosaic virus

N:Alternate names: replication-associated protein

C:Species: Indian cassava mosaic virus

C>Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 20-Sep-1999

C:Accession: JQ2327; S35883

R:Hong, Y.G.; Robinson, D.J.; Harrison, B.D.

J. Gen. Virol. 74, 2437-2443, 1993

A:Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-tr

A:Reference number: JQ2326; MUID:94065670; PMID:8245859

A:Accession: JQ2327

A:Molecule type: DNA

A:Residues: 1-351 <HON>

A:Cross-references: EMBL:Z24758; NID:G395351; PIDN:CAA80891.1; PID:G584046

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.8%; Score 216; DB 2; Length 351;

Best Local Similarity 61.2%; Pred. No. 1e-17;

Matches 41; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 4 WGFQVDSARGCGCQTSNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNLDRI 63

DB 113 WGFQIDGRSARGGQQTANDAYAAALNSGSKSEALKILRELAPRDYVLFHFHNSNLDRI 172

QY 64 FDKTPEP 70

DB 173 FTKPPPP 179

#### RESULT 11

QYCVMI

AVI protein - abutilon mosaic virus (isolate West India)

C:Species: abutilon mosaic virus

C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 08-Apr-1994

C:Accession: A36214

R:Frischmuth, T.; Zimmatt, G.; Jeske, H.

Virology 178, 461-468, 1990

A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as

A:Reference number: A36214; MUID:91020984; PMID:2219703

A:Accession: A36214

A:Molecule type: DNA

A:Residues: 1-355 <FRI>

A:Cross-references: EMBL:X15983

C:Genetics:

A:Map position: segment A

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match

Best Local Similarity 58.6%; Score 216; DB 1; Length 355;

Matches 41; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGCGCQTSNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNL 60

DB 110 TAEWGEFQIDGRSARGGQQTANDSVAKALNAGDVQSALNLIKKEQPKDYVLFQHNIRSNL 169

QY 61 DRIFDKTPEP 70

DB 170 ERIFAKAPEP 179

#### RESULT 12

S28360

ALI protein - beet curly top virus

```

A;Residues: 1-357 <NAV>
A;Cross-references: GB:X15656; NID:G62204; PIDN:CAA33688.1; PID:G62207
C;Superfamily: tomato golden mosaic virus A11 protein

Query Match          55.4%; Score 200; DB 1; Length 357;
Best Local Similarity 63.9%; Pred. No. 8e-16;
Matches 39; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY  4 WGEFQVDRSARGGCQTSDNDAAEALNASSKEEALQIITAAAIPEKYLQFHNLNSLDRI 63
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  111 FGVSQIDGRSARGGQQSANDAYAEALNSGSKSEALNLIKERAKPDYIIQFHNLNSLDRI 170

QY  64 P 64
Db  171 F 171

RESULT 15
S59885
replication-associated protein C1 - tomato yellow leaf curl virus
C;Species: tomato yellow leaf curl virus
C;Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
C;Accession: S59885
R;Hong, Y.; Harrison, B.D.
submitted to the EMBL Data Library, February 1995
A;Description: Nucleotide sequences from tomato leaf curl viruses from different
d geminiviruses.
A;Reference number: S58346
A;Accession: S59885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <HON>
A;Cross-references: EMBL:Z48182; NID:G944838; PIDN:CAA88229.1; PID:G974211
C;Superfamily: tomato golden mosaic virus A11 protein

Query Match          55.1%; Score 199; DB 2; Length 360;
Best Local Similarity 57.6%; Pred. No. 1.1e-15;
Matches 38; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY  4 WGEFQVDRSARGGCQTSDNDAAEALNASSKEEALQIITAAAIPEKYLQFHNLNSLDRI 63
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  113 FGVSQIDGRSARGGQQSANDAYAEALNSGSKAAALDILREKAPKDFVQLQFHNLNANLDRI 172

QY  64 PDKTPE 69
Db  173 FTPSAE 178

Search completed: December 23, 2003, 09:05:20
Job time : 11 secs

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds  
(without alignments)  
569.747 Million cell updates/sec

Title: US-09-289-346B-4

Perfect score: 361

Sequence: 1 TLVWGEFQVDRSARGGCGT.....PQFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	95.8	352	1 VAL1_TGMV	P03567 tomato gold
2	249	69.0	361	1 VAL1_PYMV	P27258 potato yell
3	240	66.5	358	1 VAL1_CLVK	P14982 cassava lat
4	240	66.5	358	1 VAL1_CLVN	P14972 cassava lat
5	233	64.5	362	1 VAL1_TYLCU	P36279 tomato yell
6	229	63.4	359	1 VAL1_TYLCU	P38609 tomato yell
7	222	61.5	349	1 VAL1_PHVU	Q06923 pepper huas
8	222	61.5	359	1 VAL1_TYLCU	P27260 tomato yell
9	217	60.1	353	1 VAL1_BGMV	P05175 bean golden
10	216	59.8	355	1 VAL1_ABMVW	P21947 abutilon mo
11	213	59.0	358	1 VAL1_ECTV	P14991 beet curly
12	210	58.2	361	1 VAL1_TMOV	Q06657 tomato mott
13	200	55.4	357	1 VAL1_TYLCV	P27259 tomato yell
14	128	35.5	347	1 VAL1_SLCV	P29048 squash leaf
15	61.5	17.0	299	1 Y175_HELPU	Q92mg7 helicobacte
16	61.5	17.0	334	1 G3P_BACST	P00362 bacillus st
17	61.5	17.0	335	1 G3P_BACCO	P15115 bacillus co
18	61.5	17.0	1044	1 BUB1_SCHPO	Q04751 schizosacch
19	60	16.6	1008	1 YX4_SCHPO	Q9uu99 schizosacch
20	59	16.3	1502	1 CYP1_YEAST	P12351 saccharomyc
21	58.5	16.2	297	1 RRPB_RABVP	P06747 rabies viru
22	58	16.1	492	1 MOT3_MOUSE	Q35308 mus musculu
23	58	16.1	492	1 MOT3_RAT	O70461 rattus norv
24	58	16.1	555	1 GLPD_BACSU	P18158 bacillus su
25	58	16.1	601	1 CYSJ_BUCAI	P57503 buchnera ap
26	57.5	15.9	396	1 DXR_XANAC	Q8pml1 xanthomonas
27	57	15.8	223	1 DGK2_LACAC	O59484 lactobacill
28	57	15.8	316	1 SPDE_COPAR	O82147 coffea arab
29	57	15.8	379	1 CYB_ASTPE	Q33818 asterina pe
30	57	15.8	387	1 Y4PF_RHISN	P55615 rhizobina s
31	57	15.8	836	1 GCSR_HUMAN	Q99062 homo sapien
32	57	15.8	1287	1 SKI2_YEAST	P35207 saccharomyc
33	56.5	15.7	863	1 AMEN_CAUCR	P37893 caulobacter

34 56 15.5 367 1 LHX4\_MOUSE P53776 mus musculu  
35 56 15.5 476 1 DGRH\_HUMAN Q96df8 homo sapien  
36 56 15.5 479 1 DGRH\_MOUSE O70279 mus musculu  
37 56 15.5 577 1 PTLB\_LACCA P24400 lactobacill  
38 56 15.5 874 1 SLAP\_BACLI P49052 bacillus li  
39 55.5 15.4 298 1 OLG2\_CHICK Q90xb3 gallus gall  
40 55.5 15.4 299 1 Y175\_HELPU P56112 helicobacte  
41 55.5 15.4 323 1 VAL1\_PASVK Q00338 panicum str  
42 55.5 15.4 397 1 METL\_RAT P13444 rattus norv  
43 55.5 15.4 428 1 GBA1\_CANAL P28868 candida alb  
44 55.5 15.4 468 1 AMPA\_NEIMA Q91ti8 neisseria m  
45 55.5 15.4 515 1 LEU1\_BACHD Q98e8 bacillus ha

#### ALIGNMENTS

RESULT 1  
VAL1\_TGMV STANDARD; PRT; 352 AA.  
AC P03567;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE AL1 protein.  
GN AC1.  
OS Tomato golden mosaic virus (TGMV).  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=10831;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;  
RT "Complete nucleotide sequence of the infectious cloned DNA components of tomato golden mosaic virus: potential coding regions and regulatory sequences."  
RL EMBO J. 3:2197-2205(1984).  
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.  
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CC -----  
DR PIR; A04170; Q0CVL1; NOT\_ANNOTATED\_CDS.  
DR InterPro; IPR001191; Gemini\_AL1.  
DR Pfam; PF00799; Gemini\_AL1.  
DR PRINTS; PR00227; GEMCOATAL1.  
DR ProDom; PD000736; Gemini\_AL1; 1.  
KW ATP-binding.  
FT NP BIND 223 230 ATP (POTENTIAL).  
SQ SEQUENCE 352 AA; 40332 MW; C33C938S9644B44 CRC64;  
Query Match 95.8%; Score 346; DB 1; Length 352;  
Best Local Similarity 95.7%; Pred. No. 2.3e-34;  
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TLVWGEFQVDRSARGGCGTSDNDAALNASSKEEALQITAAAIPEKYLQFHNLSNL 60  
DB 111 TLVWGEFQVDRSARGGCGTSDNDAALNASSKEEALQITREIKPEKYLQFHNLSNL 170  
QY 61 DRIFDKTPEP 70  
DB 171 DRIFDKTPEP 180  
RESULT 2  
VAL1\_PYMV STANDARD; PRT; 361 AA.  
ID VAL1\_PYMV  
AC P27258;

```

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
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CC -----
DR EMBL; D00940; BAA00782.1; -.
DR PIR; J00364; QOCVPT.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
KW NP-BIND.
FT NP-BIND. 222 229 ATP (POTENTIAL).
SQ SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;

Query Match
Best Local Similarity 69.0%; Score 249; DB 1; Length 361;
Matches 47; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGRGCGQTSNDAAAEALNASKKEALQIIAAAIPEKYLFOPHNLNSNL 60
Db 110 TIEWGLFQIDGRSGRGCGQTSNDAAAEALNASKKEALQIIAAAIPEKYLFOPHNLNSNL 169

QY 61 DRIFDKTPE 69
Db 170 DRIFDKAPE 178

RESULT 3
VAL1_CLVK
ID VAL1_CLVK STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RX Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA."
RL Nature 301:260-262(1983).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP-BIND. 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753BE92D69 CRC64;

Query Match
Best Local Similarity 66.5%; Score 240; DB 1; Length 358;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGRGCGQTSNDAAAEALNASKKEALQIIAAAIPEKYLFOPHNLNSNL 60
Db 109 TVEWGQFQIDGRSGRGCGQTSNDAAAEALNASKKEALQIIAAAIPEKYLFOPHNLNSNL 168

QY 61 DRIFDKTPE 70
Db 169 DRIFQEPAP 178

RESULT 4
VAL1_CLVN
ID VAL1_CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain)."
RL Nucleic Acids Res. 18:197-198(1990).
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CC -----
DR EMBL; X17095; CAA34953.1; -.
DR PIR; S07594; S07594.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP-BIND. 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16BB0CB2D5E2C CRC64;

Query Match
Best Local Similarity 66.5%; Score 240; DB 1; Length 358;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGRGCGQTSNDAAAEALNASKKEALQIIAAAIPEKYLFOPHNLNSNL 60
Db 109 TVEWGQFQIDGRSGRGCGQTSNDAAAEALNASKKEALQIIAAAIPEKYLFOPHNLNSNL 168

QY 61 DRIFDKTPE 70
Db 169 DRIFQEPAP 178

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CC EMBL; Z25751; CAA81026.1; -
DR PIR; S39211; S39211.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding. 221 228 ATP (POTENTIAL).
FT NP BIND 221 228
SQ SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3EC CRC64;

Query Match 63.4%; Score 229; DB 1; Length 359;
Best Local Similarity 60.9%; Pred. No. 3.6e-20;
Matches 42; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDSRGSGCQTSDAAAEALNASSKEBALQIIAAAIPEKYLFOFHNLSNLD 61
Db 111 LHWGTFQIDGRSARGGQQTANDAYAKAINAGSKSEALDVIKELAPRDYILHFHNINSNLD 170
QY 62 RIFDKTPEP 70
Db 171 RVFQVPPAP 179

RESULT 7
ID VAL1_PHV STANDARD; PRT; 349 AA.
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
comparison with bipartite Geminiviruses.";
RL J. Gen. Virol. 74:2225-2231(1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC
CC EMBL; X70418; CAA49856.1; -
DR PIR; JQ2300; JQ2300.
DR PIR; S31875; S31875.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding. 221 228 ATP (BY SIMILARITY).
FT NP BIND 221 228
SQ SEQUENCE 349 AA; 39722 MW; D5F4E76CD56370F4 CRC64;

Query Match 61.5%; Score 222; DB 1; Length 349;
Best Local Similarity 60.0%; Pred. No. 2.4e-19;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGCQTSDAAAEALNASSKEBALQIIAAAIPEKYLFOFHNLSNLD 60
Db 110 TVWGEFQIDGRSARGGQQSANDTYAKALNSASAEALQIKEQPFHFLQFHNIVSNA 169

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CC EMBL; Z25751; CAA81026.1; -
DR PIR; S39211; S39211.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding. 221 228 ATP (POTENTIAL).
FT NP BIND 221 228
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;

Query Match 64.5%; Score 233; DB 1; Length 362;
Best Local Similarity 54.1%; Pred. No. 1.2e-20;
Matches 46; Conservative 9; Mismatches 14; Indels 16; Gaps 1;

QY 1 TLVWGEFQVDSRGSGCQTSDAAAEALNASSKEBALQIIAAAIPEKYLFOFHNLSNLD 60
Db 110 TVWGEFQIDGRSARGGQQSANDTYAKALNTGSKSEALNVRELAPKDYVLQFHNLSNLD 169
QY 61 DRI-----FDKTPPE 69
Db 170 DRIFTPPLEVYVSPFLSSSFDVRPE 194

RESULT 6
ID VAL1_TYLCU STANDARD; PRT; 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 protein (CI protein).
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Norris E., Hidalgo E., Accotto G., Moriones E.;
RA "High similarity among the tomato yellow leaf curl virus isolates
RT from the west Mediterranean basin: the nucleotide sequence of an
RT infectious clone from Spain.";
RL Arch. Virol. 135:165-170(1994).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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QY 61 DRIFDKTPEP 70
Db 170 NRIFQTPPEP 179

RESULT 8
ID VAL1 TYLCM STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, last sequence update)
DT 15-SEP-2003 (Rel. 42, last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92107660; PubMed=1840676;
RA Kheyr-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
RA Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a
RT whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
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CC -----
DR EMBL; X61153; CAA43466.1; -.
DR PIR; S22593; S22593.
DR PDB; 1L2M; 18-SEP-02.
DR PDB; 1L5I; 18-SEP-02.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding; 3D-structure.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 40733 MW; 9717B4A07C93EFA7 CRC64;

Query Match 61.5%; Score 222; DB 1; Length 359;
Best Local Similarity 58.0%; Pred. No. 2.5e-19;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDRSGCGCOTSDAAEAALNASSKEEALQIAAIAPEKYLFOFHNLNSLD 61
Db 111 LEWGTFOIDGSRAGGQQTANDAYAKAINAGSKQALDVIKELAPRDYVLHFNHNSLD 170

QY 62 RIFDKTPEP 70
Db 171 KVFPVPPAP 179

RESULT 9
ID VAL1 BGMV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, last sequence update)
DT 01-OCT-1996 (Rel. 34, last annotation update)
DE AL1 protein (40.2 kDa protein).
GN AC1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RA Howarth A.J., Caton J., Bossert M., Goodman R.M.;
RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
RT regulation in geminiviruses";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
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CC -----
DR EMBL; M10070; AAA46318.1; -.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 60.1%; Score 217; DB 1; Length 353;
Best Local Similarity 60.0%; Pred. No. 1e-18;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLWGEFQVDRSGCGCOTSDAAEAALNASSKEEALQIAAIAPEKYLFOFHNLNSNL 60
Db 110 TIENGQFQVDRSGAGGQQTANDAYAKAINAGSKQALDVILKERQPKDYVLQNHNRSLN 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFPKTPEP 179

RESULT 10
ID VAL1 ABMV STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, last sequence update)
DT 01-JUN-1994 (Rel. 29, last annotation update)
DE AL1 protein.
GN AC1.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimmat G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; X15983; -. NOT_ANNOTATED_CDS.
DR PIR; A36214; QQCVM1.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
ATP-binding.
KW
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FT NP BIND 221 228 ATP (POTENTIAL)
SQ SEQUENCE 355 AA; 40257 MW; 16A2CAGA63251E95 CRC64;

Query Match
Best Local Similarity 59.8%; Score 216; DB 1; Length 355;
Matches 41; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSRGCGCQTSDNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNL 60
DB 110 TAEWGFQVDSRGCGCQTSDNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNL 169

QY 61 DRIFDKTPPEP 70
DB 170 ERIFAKAPEP 179

RESULT 11
VAL1_BCTV STANDARD; PRT; 358 AA.
AC P14991;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein (40.8 kDa protein).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
RT beet curly top virus";
RL EMBO J. 5:1761-1767(1986).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
CC EMBL; X04144; -; NOT ANNOTATED CDS.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATL1.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
CC NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;

Query Match
Best Local Similarity 59.0%; Score 213; DB 1; Length 358;
Matches 39; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSRGCGCQTSDNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNL 60
DB 110 TIEWGFQVDSRGCGCQTSDNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNL 169

QY 61 DRIFDKTPPEP 70
DB 170 QKIFQPPDP 179

RESULT 12
VAL1_TMOV STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.

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GN AL1.
OC Tomato mottle virus (isolate Florida) (TMOV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93107858; PubMed=1469361;
RA Abousaid A.M., Polston J.E., Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida.";
RL J. Gen. Virol. 73:3225-3229(1992).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
CC EMBL; L14460; AAC32414.1; -
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATL1.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
CC NP BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 8138B65CEBAC6950 CRC64;

Query Match
Best Local Similarity 58.2%; Score 210; DB 1; Length 361;
Matches 38; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSRGCGCQTSDNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNL 60
DB 110 TIEWGFQVDSRGCGCQTSDNDAAAEALNASKEEALQIIAAAIPEKYLFOFHNLSNL 169

QY 61 DRIFDKTPPEP 70
DB 170 ERIFAKAPEP 179

RESULT 13
VAL1_TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OC Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92024070; PubMed=1926771;
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component.";
RL Virology 185:151-161(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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Qy      5    GETQVDRSGRCQTSDNAAEALNASKEEALQIIAAAIPEKYLFOPHNINSNLDRIF    64  
Db       |     :     |     |     |     |     |     |     |     |     |     |     |     |  
         |     :     |     |     |     |     |     |     |     |     |     |     |  
116    GQYKVSQ-----GSKSNKKDDVYHNNAVNSAGSAGEALDIKAGDPKTFIVNYHNLANVERLF    171

Qy                  65    DKTPPEP    70  
                     |     |     |     |  
Db                  172    QKPPEP    177

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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 25.3333 Seconds  
(without alignments)  
713.040 Million cell updates/sec

Title: US-09-289-346b-4  
Perfect score: 361  
Sequence: 1 TLVWGEFQVDRSGRGSCQT.....FQFHLNLSNLDRIFDKTPPEP 70

Scoring table: BLOSUM62

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297	82.3	351	12	Q91R10 tomato seve
2	295	81.7	352	12	Q9E000
3	290	80.3	232	12	Q8QV33 tomato rugo
4	281	77.8	226	12	Q9WHF6 tomato chlo
5	281	77.8	226	12	Q9WHF6 tomato mild
6	279	77.3	361	12	Q09727 leonurus mo
7	277	76.7	225	12	Q67574 bean golden
8	274	75.9	314	12	Q9QDB1 cowpea gold
9	274	75.9	364	12	Q9ELT8 sweet potat
10	271	75.1	185	12	Q9Q555 sweet potat
11	270	74.8	235	12	Q98693 sida golden
12	269	74.5	208	12	Q8QPU4 tomato infe
13	269	74.5	289	12	Q8JLY3 potato yell
14	266	73.7	149	12	Q8JLY5 potato yell
15	266	73.7	233	12	P88975 macroptiliu
16	265	73.4	361	12	Q9YLA4 macroptiliu
					Q8JMJ4 potato yell

17	261	72.3	361	12	Q8QVH0
18	260	72.0	234	12	Q39180
19	260	72.0	360	12	Q8QMH4
20	255	70.6	223	12	Q8QPU7
21	255	70.4	190	12	Q8Z089
22	254	70.4	190	12	Q8Z084
23	253	70.1	190	12	Q9W827
24	253	70.1	208	12	Q9Z0C4
25	253	70.1	359	12	Q91M88
26	253	70.1	359	12	Q8JVE8
27	251	69.5	208	12	Q9Z0C0
28	251	69.5	208	12	Q9Z0B8
29	251	69.5	363	12	Q72719
30	251	69.5	363	12	Q72705
31	249	69.0	208	12	Q9Z0B6
32	248	68.7	203	12	Q9Z083
33	248	68.7	359	12	Q9YZV4
34	248	68.7	359	12	Q9YUX7
35	248	68.7	359	12	Q9YL27
36	248	68.7	359	12	Q9YZV2
37	248	68.7	363	12	Q73577
38	247	68.4	359	12	Q8JNG3
39	247	68.4	359	12	Q88942
40	245	67.9	307	12	Q91ET7
41	245	67.9	361	12	Q72723
42	245	67.9	363	12	Q8JLK6
43	244	67.6	348	12	Q91LW5
44	243	67.3	359	12	Q91B86
45	243	67.3	360	12	Q9DX10

ALIGNMENTS

RESULT 1

Q91R10 ID Q91R10 PRELIMINARY; PRT; 351 AA.  
AC Q91R10;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Rep protein.  
GN ACl.  
OS Tomato severe rugose virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=158463;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Minas Gerais;  
RA Rezende W.L., Goulart L.R., Parreira K.S., Figueiredo J.E.F.;  
RT "The full-length DNA-A nucleotide sequence of a novel tomato-infecting  
RL begomovirus, Tomato severe rugose virus, in Brazil."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY029750; AAK50357.1;  
DR InterPro; IPR001191; Gemini\_A11.  
DR Pfam; PF00799; Gemini\_A11; 1.  
DR PRINTS; PR00227; GEMCOAT11.  
DR ProDom; PD000736; Gemini\_A11; 1.  
SQ SEQUENCE 351 AA; 40122 MW; 87F937A4F873B6CF CRC64;

Query Match 82.3%; Score 297; DB 12; Length 351;  
Best Local Similarity 78.6%; Pred. No. 1.7e-27;  
Matches 55; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy	1	TLVWGEFQVDRSGRGSCQTNDAAAEALNASKEEALQIIAAAIPEKYLFOFHLNLSNL 60
Db	111	TIWGEFQIDRGARGCGCFANDAAAEALNAPSQVALQIIREKLPKFLFOFHLNLSNL 170
Qy	61	DRIFDKTPPEP 70
Db	171	DRIFARAPEP 180





[illegible]

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QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 9
Q98555 PRELIMINARY; PRT; 364 AA.
AC Q98555;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Replication initiation protein Acl.
GN Acl.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De la Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RN Plant Dis. 82:1253-1257(1998).
[2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RT virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0(1999).
DR EMBL: AF104036; AAD47173.1; -.
DR InterPro: IPR001191; Gemini AL1.
DR Pfam: PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRODOM; PD000736; Gemini AL1; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 75.98; Score 274; DB 12; Length 364;
Best Local Similarity 79.48; Pred. No. 1.1e-24;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGCGCOTSDAAAEALNASSKEEALQIIAAAIPEKYLQFPHNLNSNL 60
Db 110 TITWGEFQVDRSGCGCQTANDAAAEALNASSKEEALQIIREKLPKYLQFPHNLVSNL 169

QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN Acl.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA Royle M.E., McLaughlin W.A., Nakhla N.K., Maxwell D.P.;
RT "Genetic Diversity among geminiviruses associated with the weed
RT species Sida spp, Macroptilium lathyroides, and Wissadula amplusima
RT from Jamaica.";
RL Plant Dis. 81:1251-1258(1997).
DR EMBL: U67926; AAB97865.1; -.
DR InterPro: IPR001191; Gemini AL1.
DR Pfam: PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.

QY 61 DRIFDKTP 70
Db 173 FTKAPDP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN Acl.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

DR PRODOM; PD000736; Gemini AL1; 1.
FT NON_TER 1
SQ SEQUENCE 185 AA; 20975 MW; 3913850A025A5BE1 CRC64;

Query Match 75.1%; Score 271; DB 12; Length 185;
Best Local Similarity 70.0%; Pred. No. 1.1e-24;
Matches 49; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGCGCOTSDAAAEALNASSKEEALQIIAAAIPEKYLQFPHNLNSNL 60
Db 89 TIEWGVQIDGRSGRGCGQTANDAAAEALNASSKEEALQIIREKLPKYLQFPHNLSSNI 148

QY 61 DRIFDKTP 70
Db 149 DRIFSKPPPP 158

RESULT 11
Q8QP4 PRELIMINARY; PRT; 235 AA.
AC Q8QP4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN Acl.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG-B11;
RA Ribeiro S.G., Ambrozovicus L.P., de Avila A.C., Calegario R.F.,
RT Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY049208; AAL82833.1; -.
DR InterPro: IPR001191; Gemini AL1.
DR Pfam: PF00799; Gemini AL1; 1.
DR PRODOM; PD000736; Gemini AL1; 1.
FT NON_TER 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BE0DD9C810 CRC64;

Query Match 74.8%; Score 270; DB 12; Length 235;
Best Local Similarity 74.8%; Pred. No. 1.9e-24;
Matches 50; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 4 WGEFQVDRSGCGCOTSDAAAEALNASSKEEALQIIAAAIPEKYLQFPHNLNSLDRI 63
Db 113 WGIFQIDGRSGRGCGQTANDAAAEALNASSKEEAMQIIKEKLPKYLQFPHNLSCNLDRI 172

QY 64 FDKTTP 70
Db 173 FTKAPDP 179

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RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126611; AAM95995.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF007799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 208 208
SQ SEQUENCE 208 AA; 23667 MW; 51211D58FAD690A6 CRC64;

Query Match 74.5%; Score 269; DB 12; Length 208;
Best Local Similarity 71.4%; Pred. No. 2.2e-24;
Matches 50; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 60
Db 110 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 169

QY 61 DRFDKTPPEP 70
Db 170 DRIFWKAPEP 179

RESULT 13
Q8JLY5 PRELIMINARY; PRT; 289 AA.
AC Q8JLY5;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;
RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126610; AAM95993.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF007799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 289 289
SQ SEQUENCE 289 AA; 32971 MW; 4ECF52F4C69C6764 CRC64;

Query Match 74.5%; Score 269; DB 12; Length 289;
Best Local Similarity 71.4%; Pred. No. 3.3e-24;
Matches 50; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 60
Db 110 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 169

QY 61 DRFDKTPPEP 70
Db 170 DRIFWKAPEP 179

RESULT 14
P88975 PRELIMINARY; PRT; 149 AA.
AC P88975;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;

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RN SEQUENCE FROM N.A.
RP STRAIN=Jamaican;
RA Roye M.E.;
RL Thesis (1996), Biochemistry, University of the West Indies, Jamaica.
DR EMBL; U75278; AAB36919.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF007799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16785 MW; E4CF5EED4C9CD508 CRC64;

Query Match 73.7%; Score 266; DB 12; Length 149;
Best Local Similarity 70.0%; Pred. No. 3.4e-24;
Matches 49; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 60
Db 52 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 111

QY 61 DRFDKTPPEP 70
Db 112 DRIFWKAPEP 121

RESULT 15
Q9YLA4 PRELIMINARY; PRT; 233 AA.
AC Q9YLA4;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica strain 1;
RA Roye M.E.;
RT "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica strain 1;
RA Roye M.E., McLaughlin W.A., Maxwell D.P.;
RT "Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098940; AAD17850.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF007799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 233 233
SQ SEQUENCE 233 AA; 26356 MW; AA490AF4D2166A02 CRC64;

Query Match 73.7%; Score 266; DB 12; Length 233;
Best Local Similarity 70.0%; Pred. No. 5.9e-24;
Matches 49; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 60
Db 110 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEALQITAAAIPEKYLFOFHNLSNL 169

QY 61 DRFDKTPPEP 70
Db 170 DRIFWKAPEP 179

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Search completed: December 23, 2003, 09:03:35  
Job time : 25.3333 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds  
(without alignments)  
340.128 Million cell updates/sec

Title: US-09-289-346B-5  
Perfect score: 359  
Sequence: 1 TLVWGFQYDGRSARGCQT.....FQPHNLNSMLDRFDKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :			
A: Geneseq_19Jun03.*			
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2:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*		
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22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*		
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359	100.0	70	21	AA198681
2	343	95.5	70	21	AA198677
3	343	95.5	356	21	AA198687
4	335	93.3	70	21	AA198685
5	332	92.5	70	21	AA198688
6	331	92.2	70	21	AA198692
7	329	91.6	70	21	AA198684
8	329	91.6	70	21	AA198690
9	328	91.4	70	21	AA198678

10	328	91.4	70	21	AA198686	Mutant peptide der
11	327	91.1	70	21	AA198689	Mutant peptide der
12	325	90.5	70	21	AA198680	Mutant peptide der
13	325	90.5	70	21	AA198691	Mutant peptide der
14	321	89.4	70	21	AA198683	Mutant peptide der
15	319	88.9	70	21	AA198682	Mutant peptide der
16	311	86.6	70	21	AA198679	Mutant peptide der
17	220	61.3	361	18	AAW34336	Tomato mottle viru
18	220	61.3	361	18	AAW34324	Tomato mottle viru
19	220	61.3	361	18	AAW34325	Tomato mottle viru
20	220	61.3	361	18	AAW34326	Tomato mottle viru
21	219	61.0	359	17	AAW34327	Sardinian tomato y
22	219	61.0	359	17	AAW34328	Sardinian tomato y
23	219	61.0	359	17	AAW34329	Sardinian tomato y
24	218	60.7	353	18	AAW34330	Bean golden mosaic
25	218	60.7	353	18	AAW34331	Bean golden mosaic
26	218	60.7	353	18	AAW34332	Bean golden mosaic
27	218	60.7	353	18	AAW34333	Bean golden mosaic
28	218	60.7	353	18	AAW34334	Bean golden mosaic
29	216	60.2	353	8	AAW34335	ORF 4 gene product
30	208.5	58.1	361	8	AAW34336	Product of ORF 4 f
31	208	57.9	362	19	AAW34337	Tobacco leaf curl
32	203	56.5	357	18	AAW34338	Tomato yellow leaf
33	203	56.5	357	18	AAW34339	Tomato yellow leaf
34	203	56.5	357	18	AAW34340	Tomato yellow leaf
35	202.5	56.4	50	23	AAW34341	Retinoblastoma-bin
36	195	54.3	357	18	AAW34342	Tomato yellow leaf
37	104	29.0	142	24	AAW34343	Tomato yellow leaf
38	66.5	18.5	512	19	AAW34344	HIV-1 strain YBF30
39	65.5	18.2	665	22	AAW34345	Drosophila melanog
40	63.5	17.7	1693	21	AAW34346	Human laminin 5 po
41	63.5	17.7	1693	21	AAW34347	Human laminin 5 po
42	63.5	17.7	1713	16	AAW34348	Human laminin 5 po
43	63.5	17.7	1713	21	AAW34349	Deduced sequence o
44	63.5	17.7	1724	21	AAW34350	Human laminin 5 po
45	63	17.5	599	22	AAW34351	Novel human diagno

ALIGNMENTS

RESULT 1	
A..198681	
ID	AA198681 standard; peptide; 70 AA.
AC	AA198681;
XX	
XX	
DT	22-JAN-2001 (first entry)
XX	
DE	Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX	
KW	Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW	ribosome binding region; resistance; geminivirus infection.
XX	
OS	Synthetic.
OS	Tomato golden mosaic virus.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 47
FT	/note= "wild type residue replaced with Ala"
FT	Misc-difference 48
FT	/note= "wild type residue replaced with Ala"
FT	Misc-difference 49
FT	/note= "wild type residue replaced with Ala"
XX	
XX	WO2000054573-A1.
XX	
PD	21-SEP-2000.
XX	
PF	15-MAR-2000; 2000WO-US06759.
XX	
PR	18-MAR-1999; 99US-0125004.
PR	09-APR-1999; 99US-0289346.

```

XX PA (UUNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PS
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PS
XX PS Claim 52; Page 44; 73pp; English.
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
XX Query Match 100.0%; Score 359; DB 21; Length 70;
XX Best Local Similarity 100.0%; Pred. No. 5e-39;
XX Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDCRSARGCGQTSNDAAEALNASSKEEALQIIREKIPAAALQFHNLSNL 60
DB 1 TLVWGEFQVDCRSARGCGQTSNDAAEALNASSKEEALQIIREKIPAAALQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 2
AAB18677
ID AAB18677 standard; peptide; 70 AA.
AC AAB18677;
XX 22-JAN-2001 (first entry)
DE Peptide fragment from Rep protein of TGMV (amino acids 110-179).
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Tomato golden mosaic virus.
XX WO200054573-Al.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UUNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PS
XX PS Disclosure; Page 18; 73pp; English.
XX CC The present sequence is derived from a geminivirus replication (Rep)
XX CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
XX CC catalyzes cleavage and ligation of single-stranded DNA, and interacts
XX CC with other viral and host proteins. Mutants of the AL1 protein are used
XX CC to produce transgenic plants. The mutation in AL1 is present in a
XX CC ribosome binding region, and expression of mutant AL1 protein imparts
XX CC increased resistance to geminivirus infection in the plant. Mutant AL1
XX CC proteins are useful for producing plants having increased resistance or
XX CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
XX CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
XX CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
XX CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
XX CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
XX CC beet curly top virus.
XX SQ Sequence 70 AA;
XX Query Match 95.5%; Score 343; DB 21; Length 70;
XX Best Local Similarity 95.7%; Pred. No. 6.1e-37;
XX Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDCRSARGCGQTSNDAAEALNASSKEEALQIIREKIPAAALQFHNLSNL 60
DB 1 TLVWGEFQVDCRSARGCGQTSNDAAEALNASSKEEALQIIREKIPAAALQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 3
AAB18687
ID AAB18687 standard; peptide; 356 AA.
XX AAB18687;
XX 22-JAN-2001 (first entry)
DE Amino acid sequence of a geminivirus replication protein of TGMV.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Tomato golden mosaic virus.
XX Key Location/Qualifiers
XX FT Misc-difference 354 /note= "unspecified amino acid"
XX WO200054573-Al.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UUNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT Transgenic plants with increased resistance to geminivirus infection

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PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX  
 XX  
 PS Disclosure; Page 47-48; 73pp; English.  
 XX  
 CC The present sequence represents a geminivirus replication (Rep)  
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,  
 CC catalyses cleavage and ligation of single-stranded DNA, and interacts  
 CC with other viral and host proteins. Mutants of the AL1 protein are used  
 CC to produce transgenic plants. The mutation in AL1 is present in a  
 CC ribosome binding region, and expression of mutant AL1 protein imparts  
 CC increased resistance to geminivirus infection in the plant. Mutant AL1  
 CC proteins are useful for producing plants having increased resistance or  
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,  
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl  
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato  
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,  
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or  
 CC beet curly top virus.  
 XX  
 SQ Sequence 356 AA;  
 Query Match 95.5%; Score 343; DB 21; Length 356;  
 Best Local Similarity 95.7%; Pred. No. 5.3e-36;  
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 TLVGEFQVDSARGGCGTSDNDAAEALNASSKEALQIREKIPAAALFQFHNLSNL 60  
 DB 110 TLVGEFQVDSARGGCGTSDNDAAEALNASSKEALQIREKIPAAALFQFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 170 DRIFDKTPEP 179  
 RESULT 4  
 AAB18685  
 ID AAB18685 standard; peptide; 70 AA.  
 XX  
 AC AAB18685;  
 DT 22-JAN-2001 (first entry)  
 XX  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX  
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 10 /note= "wild type residue replaced with Ala"  
 XX  
 XX WO200054573-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 XX  
 XX 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX  
 XX Transgenic plants with increased resistance to geminivirus infection  
 XX comprise a nucleic acid construct containing a nucleic acid sequence

PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT  
 XX  
 PS Claim 53; Page 46; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;  
 Query Match 93.3%; Score 335; DB 21; Length 70;  
 Best Local Similarity 94.3%; Pred. No. 6.8e-36;  
 Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TLVGEFQVDSARGGCGTSDNDAAEALNASSKEALQIREKIPAAALFQFHNLSNL 60  
 DB 1 TLVGEFQVDSARGGCGTSDNDAAEALNASSKEALQIREKIPAAALFQFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 5  
 AAB18688  
 ID AAB18688 standard; peptide; 70 AA.  
 XX  
 AC AAB18688;  
 XX  
 DT 22-JAN-2001 (first entry)  
 XX  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX  
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 19 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 20 /note= "wild type residue replaced with Ala"  
 XX  
 XX WO200054573-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 XX  
 XX 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX  
 XX Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 PS Disclosure; Page 48; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;

Query Match 92.5%; Score 332; DB 21; Length 70;  
 Best Local Similarity 92.3%; Pred. No. 1.7e-35;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGARGCGCOTSDAAAEALNASSKEEALQIIRKIPAAALFQPHNLSNL 60  
 |||||  
 DB 1 TLVWGFQVDRSGARGCGCOTSDAAAEALNASSKEEALQIIRKIPAAALFQPHNLSNL 60

QY 61 DRIFDKTPEP 70  
 |||||  
 DB 61 DRIFDKTPEP 70

RESULT 6  
 AAB18692  
 ID AAB18692 standard; peptide; 70 AA.  
 AC AAB18692;  
 DT 22-JAN-2001 (first entry)  
 XX  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 66 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"  
 FT  
 XX WO200054573-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 XX 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.

PT Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Disclosure; Page 50; 73pp; English.  
 PS  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;

Query Match 92.2%; Score 331; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 2.3e-35;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGARGCGCOTSDAAAEALNASSKEEALQIIRKIPAAALFQPHNLSNL 60  
 |||||  
 DB 1 TLVWGFQVDRSGARGCGCOTSDAAAEALNASSKEEALQIIRKIPAAALFQPHNLSNL 60

QY 61 DRIFDKTPEP 70  
 |||||  
 DB 61 DRIFDKTPEP 70

RESULT 7  
 AAB18684  
 ID AAB18684 standard; peptide; 70 AA.  
 AC AAB18684;  
 DT 22-JAN-2001 (first entry)  
 XX  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 7 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"  
 FT  
 XX WO200054573-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 XX 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.



XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT  
 XX  
 PS Claim 52; Page 45; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;  
 Query Match 91.6%; Score 329; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 4.1e-35;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDSARGCGCQTSNDAAALNASSKEEALQIIREKIPAAALFQPHNLNSNL 60  
 DB 1 TLVWGEFQVDSARGCGCQTSNDAAALNASSKEEALQIIREKIPAAALFQPHNLNSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 8  
 AAB18690  
 ID AAB18690 standard; peptide; 70 AA.  
 AC AAB18690;  
 XX  
 XX 22-JAN-2001 (first entry)  
 DT  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 XX Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 27 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 30 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 30 /note= "wild type residue replaced with Ala"  
 FT  
 XX WO200054573-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 PA Hanley-Bowdoin L, Orozco BM, Kong L;  
 PI  
 XX

DR WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT  
 XX  
 PS Disclosure; Page 49; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;  
 Query Match 91.6%; Score 329; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 4.1e-35;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDSARGCGCQTSNDAAALNASSKEEALQIIREKIPAAALFQPHNLNSNL 60  
 DB 1 TLVWGEFQVDSARGCGCQTSNDAAALNASSKEEALQIIREKIPAAALFQPHNLNSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 9  
 AAB18678  
 ID AAB18678 standard; peptide; 70 AA.  
 AC AAB18678;  
 XX  
 XX 22-JAN-2001 (first entry)  
 DT  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 XX Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 12 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 13 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 15 /note= "wild type residue replaced with Ala"  
 FT  
 XX WO200054573-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 PA

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XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX PA WPI; 2000-618851/59.
XX DR
XX XX Transgenic plants with increased resistance to geminivirus infection
XX FT comprise a nucleic acid construct containing a nucleic acid sequence
XX FT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX FT
XX PS Claim 53; Page 42-43; 73pp; English.
XX CC
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 91.4%; Score 328; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 5.6e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 TLVWGEFQVDRSGRGCGQTNDAAAEALNASKEEALQIIREKIPAAALFQFHNLSNL 60
Db 1 TLVWGEFQVDRSGRGCGQTNDAAAEALNASKEEALQIIREKIPAAALFQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 10
AAB18686
ID AAB18686 standard; peptide; 70 AA.
AC AAB18686;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 24 /note= "wild type residue replaced with Leu"
XX FT Misc-difference 25 /note= "wild type residue replaced with Leu"
XX FT Misc-difference 26 /note= "wild type residue replaced with Leu"
XX FT
XX WO200054573-A1.
XX PN
XX 21-SEP-2000.
XX PD
XX 15-MAR-2000; 2000WO-US06759.
XX PF
XX 18-MAR-1999; 99US-0125004.
XX PR

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PR 09-APR-1999; 99US-0289346.
XX
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX FI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX XX Transgenic plants with increased resistance to geminivirus infection
XX FT comprise a nucleic acid construct containing a nucleic acid sequence
XX FT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX FT
XX PS Claim 53; Page 46; 73pp; English.
XX CC
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 91.4%; Score 328; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 5.6e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 TLVWGEFQVDRSGRGCGQTNDAAAEALNASKEEALQIIREKIPAAALFQFHNLSNL 60
Db 1 TLVWGEFQVDRSGRGCGQTNDLLLEALNASKEEALQIIREKIPKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 11
AAB18689
ID AAB18689 standard; peptide; 70 AA.
AC AAB18689;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 22 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX FT
XX WO200054573-A1.
XX PN
XX 21-SEP-2000.
XX PD
XX 15-MAR-2000; 2000WO-US06759.
XX PF
XX
XX

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PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
DR WPI; 2000-618851/59.
XX
PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
PS Disclosure; Page 48-49; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 91.1%; Score 327; DB 21; Length 70;
Best Local Similarity 92.9%; Pred. No. 7.5e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 TLVWGEFQVDSRGSGCQTNDAAAEALNASSKEEALQIREKIPAAALFQFHNLSNL 60
DB 1 TLVWGEFQVDSRGSGCQTNDAAAEALNASSKEEALQIREKIPAAALFQFHNLSNL 60
OY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 12
AAB18680
ID AAB18680 standard; peptide; 70 AA.
XX
AC AAB18680;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
XX OS Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 42 /note= "wild type residue replaced with Ala"
FT Misc-difference 43 /note= "wild type residue replaced with Ala"
FT Misc-difference 44 /note= "wild type residue replaced with Ala"
XX
PN W0200054573-A1.
XX
PD 21-SEP-2000.
XX

XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX
XX Claim 52; Page 43-44; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
Query Match 90.5%; Score 325; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.4e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 1 TLVWGEFQVDSRGSGCQTNDAAAEALNASSKEEALQIREKIPAAALFQFHNLSNL 60
DB 1 TLVWGEFQVDSRGSGCQTNDAAAEALNASSKEEALQIREKIPAAALFQFHNLSNL 60
OY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 13
AAB18691
ID AAB18691 standard; peptide; 70 AA.
XX
AC AAB18691;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
XX OS Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 34 /note= "wild type residue replaced with Ala"
FT Misc-difference 35 /note= "wild type residue replaced with Ala"
FT Misc-difference 36 /note= "wild type residue replaced with Ala"
XX
XX
```

PN WO200054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 PI WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT  
 XX Disclosure; Page 49; 73pp; English.  
 XX The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX Sequence 70 AA;  
 SQ  
 Query Match 90.5%; Score 325; DB 21; Length 70;  
 Best Local Similarity 91.4%; Pred. No. 1.4e-34;  
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDSARGCGCOTSDAAAEALNASSKEALQIIREKIPAAALFOFHNLSNL 60  
 Db 1 TLVWGEFQVDSARGCGCOTSDAAAEALNASSKEALQIIREKIPAAALFOFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 Db 61 DRIFDKTPEP 70  
 RESULT 14  
 AAB18683  
 ID AAB18683 standard; peptide; 70 AA.  
 XX AAB18683;  
 AC  
 XX 22-JAN-2001 (first entry)  
 DT Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 DE Ribosome binding region; resistance; geminivirus infection.  
 XX Synthetic.  
 KW Tomato golden mosaic virus.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 59 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 61 /note= "wild type residue replaced with Ala"  
 FT

FT Misc-difference 62 /note= "wild type residue replaced with Ala"  
 FT  
 XX WO200054573-A1.  
 PN 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 PI WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT  
 XX Claim 53; Page 45; 73pp; English.  
 PS The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX Sequence 70 AA;  
 SQ  
 Query Match 89.4%; Score 321; DB 21; Length 70;  
 Best Local Similarity 91.4%; Pred. No. 4.5e-34;  
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDSARGCGCOTSDAAAEALNASSKEALQIIREKIPAAALFOFHNLSNL 60  
 Db 1 TLVWGEFQVDSARGCGCOTSDAAAEALNASSKEALQIIREKIPAAALFOFHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 Db 61 AAFDKTPEP 70  
 RESULT 15  
 AAB18682  
 ID AAB18682 standard; peptide; 70 AA.  
 XX AAB18682;  
 AC  
 XX 22-JAN-2001 (first entry)  
 DT Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 DE Ribosome binding region; resistance; geminivirus infection.  
 XX Synthetic.  
 KW Tomato golden mosaic virus.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 52

```

FT  /note= "wild type residue replaced with Ala"
FT Misc-difference 54
FT  /note= "wild type residue replaced with Ala"
FT Misc-difference 55
FT  /note= "wild type residue replaced with Ala"
XX WO200054573-A1.
XX PN
XX XX
XX 21-SEP-2000.
XX PD
XX XX
XX 15-MAR-2000; 2000WO-US06759.
XX PF
XX 18-MAR-1999; 99US-0125004.
XX PR
XX 09-APR-1999; 99US-0289346.
XX XX
XX (UYN-C-) UNIV NORTH CAROLINA STATE.
XX PA
XX XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX PI
XX WPI; 2000-618851/59.
XX DR
XX XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the RB binding region
XX PT
XX _
XX XX
XX Claim 53; Page 44-45; 73pp; English.
XX PS
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX XX
SQ Sequence 70 AA;
Query Match 88.9%; Score 319; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 8.3e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDCRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPAAALFOFHLNSNL 60
Db 1 TLVWGEFQVDCRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPAAALFOFHLNSNL 60
QY 61 DRIFDKTEEP 70
Db 61 DRIFDKTEEP 70

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Search completed: December 23, 2003, 08:56:30  
Job time : 33.6667 secs



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Db      110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREBQPKDFVLQNHNRSL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFAKAPEP 179

RESULT 2
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4
; Query Match 61.3%; Score 220; DB 3; Length 361;
; Best Local Similarity 58.6%; Pred. No. 3.7e-21;
; Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy      1 TLWGFQVDGRSARGGCGTSDAAAEALNASSKEEALQIREKIPAAALFQPHNLNSNL 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREBQPKDFVLQNHNRSL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFAKAPEP 179

RESULT 3
US-08-838-151A-6
; Sequence 6, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6
; Query Match 61.3%; Score 220; DB 3; Length 361;
; Best Local Similarity 58.6%; Pred. No. 3.7e-21;
; Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy      1 TLWGFQVDGRSARGGCGTSDAAAEALNASSKEEALQIREKIPAAALFQPHNLNSNL 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREBQPKDFVLQNHNRSL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFAKAPEP 179

RESULT 4
US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8
; Query Match 61.3%; Score 220; DB 3; Length 361;
; Best Local Similarity 58.6%; Pred. No. 3.7e-21;
; Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy      1 TLWGFQVDGRSARGGCGTSDAAAEALNASSKEEALQIREKIPAAALFQPHNLNSNL 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREBQPKDFVLQNHNRSL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFAKAPEP 179
```

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; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6
; Query Match 61.3%; Score 220; DB 3; Length 361;
; Best Local Similarity 58.6%; Pred. No. 3.7e-21;
; Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy      1 TLWGFQVDGRSARGGCGTSDAAAEALNASSKEEALQIREKIPAAALFQPHNLNSNL 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREBQPKDFVLQNHNRSL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFAKAPEP 179

RESULT 4
US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8
; Query Match 61.3%; Score 220; DB 3; Length 361;
; Best Local Similarity 58.6%; Pred. No. 3.7e-21;
; Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy      1 TLWGFQVDGRSARGGCGTSDAAAEALNASSKEEALQIREKIPAAALFQPHNLNSNL 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 TIWGFQIDGRSARGGQSANDSYAKALNASSVQSALAVLREBQPKDFVLQNHNRSL 169
Qy      61 DRIFDKTPEP 70
Db      170 ERIFAKAPEP 179
```

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838,151A  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mueller, Lisa V  
; REGISTRATION NUMBER: 38,978  
; REFERENCE/DOCKET NUMBER: SVS3801P0260  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-616-5400  
; TELEFAX: 312-616-5460  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 361 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-838-151A-8

Query Match 61.3%; Score 220; DB 3; Length 361;  
Best Local Similarity 58.6%; Pred. No. 3.7e-21;  
Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLWGFEFQVDRSARGGCTSDNAAAEALNASSKEALQIIREKIPAAALFQPHNLSNL 60  
DB 110 TLWGTFQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLVHFNINSNL 169  
QY 61 DRIFDKTPEP 70  
DB 170 ERIFAKAPEP 179

RESULT 5  
US-08-809-103B-2  
; Sequence 2, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHOTOPATHOGENIC DNA VIRUS RESISTANT  
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR95/01192  
; FILING DATE: 15-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:

Query Match 61.0%; Score 219; DB 3; Length 359;  
Best Local Similarity 58.0%; Pred. No. 5e-21;  
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 LWGFEFQVDRSARGGCTSDNAAAEALNASSKEALQIIREKIPAAALFQPHNLSNL 61  
DB 111 LEWGTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLVHFNINSNL 170

; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-809-103B-2

Query Match 61.0%; Score 219; DB 3; Length 359;  
Best Local Similarity 58.0%; Pred. No. 5e-21;  
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 LWGFEFQVDRSARGGCTSDNAAAEALNASSKEALQIIREKIPAAALFQPHNLSNL 61  
DB 111 LEWGTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLVHFNINSNL 170  
QY 62 RIFDKTPEP 70  
DB 171 KVFEVPPAP 179

RESULT 6  
US-08-809-103B-4  
; Sequence 4, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHOTOPATHOGENIC DNA VIRUS RESISTANT  
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR95/01192  
; FILING DATE: 15-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-809-103B-4

Query Match 61.0%; Score 219; DB 3; Length 359;  
Best Local Similarity 58.0%; Pred. No. 5e-21;  
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 LWGFEFQVDRSARGGCTSDNAAAEALNASSKEALQIIREKIPAAALFQPHNLSNL 61  
DB 111 LEWGTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLVHFNINSNL 170



QY 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

## RESULT 7

US-08-809-103B-6  
; Sequence 6, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; APPLICATION NUMBER: WO PCT/FR95/01192  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-809-103B-6

Query Match 61.0%; Score 219; DB 3; Length 359;

Best Local Similarity 58.0%; Pred. No. 5e-21;  
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 LVMGFEQVDSRGSGGQTSNDAAEALNASSKEEALQIIREKIPAAALFQFHNLSNLD 61  
Db 111 LEMGTFQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170  
QY 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

## RESULT 8

US-08-809-103B-8  
; Sequence 8, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT

; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; APPLICATION NUMBER: WO PCT/FR95/01192  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-809-103B-8

Query Match 61.0%; Score 219; DB 3; Length 359;

Best Local Similarity 58.0%; Pred. No. 5e-21;  
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 LVMGFEQVDSRGSGGQTSNDAAEALNASSKEEALQIIREKIPAAALFQFHNLSNLD 61  
Db 111 LEMGTFQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170  
QY 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

## RESULT 9

US-08-838-151A-44  
; Sequence 44, Application US/08838151A  
; Patent No. 6291743  
; GENERAL INFORMATION:  
; APPLICANT: Stout, John T  
; APPLICANT: Luu, Hang T  
; APPLICANT: Maxwell, Douglas  
; APPLICANT: Ahlquist, Paul  
; APPLICANT: Hanson, Steve  
; TITLE OF INVENTION: Transgenic Plants Expressing Geniviruses  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
; STREET: Two Prudential Plaza, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60601

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-44

Query Match 60.7%; Score 218; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 6.7e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDRGARGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60
Db 110 TIWGFQVDRGARGGQSQSANDSYAKALNADSIESTILKEQPKDYVLQHNIRSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 11
US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Iuu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-49

Query Match 60.7%; Score 218; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 6.7e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDRGARGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60
Db 110 TIWGFQVDRGARGGQSQSANDSYAKALNADSIESTILKEQPKDYVLQHNIRSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 11
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Iuu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
```

```
QY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 12
US-08-838-151A-52
; Sequence 52, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-55

Query Match 60.7%; Score 218; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 6.7e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSARGCGQTSNDAAALNASSKEEALQIIRKIPAAALFQFHNLNSNL 60
Db 110 TIEWGQFQVDRSARGCGQTSNDAAALNASSKEEALQIIRKIPAAALFQFHNLNSNL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 14
US-08-838-151A-24
; Sequence 24, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds  
(without alignments)  
172.015 Million cell updates/sec

Title: US-09-289-346B-5  
Perfect score: 359  
Sequence: 1 TLVWGFEQVDRSARGGCT.....FQFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues  
Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	359	100.0	70	10	US-09-289-346A-5
2	343	95.5	70	10	US-09-289-346A-1
3	343	95.5	356	10	US-09-289-346A-11
4	335	93.3	70	10	US-09-289-346A-9
5	332	92.5	70	10	US-09-289-346A-12
6	331	92.2	70	10	US-09-289-346A-16
7	329	91.6	70	10	US-09-289-346A-8
8	329	91.6	70	10	US-09-289-346A-14
9	328	91.4	70	10	US-09-289-346A-2
10	328	91.4	70	10	US-09-289-346A-10
11	327	91.1	70	10	US-09-289-346A-13
12	325	90.5	70	10	US-09-289-346A-4
13	325	90.5	70	10	US-09-289-346A-15
14	321	89.4	70	10	US-09-289-346A-7
15	319	88.9	70	10	US-09-289-346A-6

16	311	86.6	70	10	US-09-289-346A-3
17	66.5	18.5	512	12	US-10-301-661A-4
18	66.5	18.5	1217	15	US-10-156-761A-13942
19	63.5	17.7	1713	15	US-10-171-311-113
20	62.5	17.4	429	12	US-10-032-585-7668
21	60.5	16.9	447	9	US-09-989-722-369
22	60.5	16.9	447	9	US-09-989-723-369
23	60.5	16.9	447	9	US-09-989-727-369
24	60.5	16.9	447	9	US-09-989-727-369
25	60.5	16.9	447	10	US-09-989-731-369
26	60.5	16.9	447	10	US-09-989-732-369
27	60.5	16.9	447	10	US-09-991-073-369
28	60.5	16.9	447	10	US-09-990-442-369
29	60.5	16.9	447	10	US-09-991-163-369
30	60.5	16.9	447	10	US-09-993-604-369
31	60.5	16.9	447	10	US-09-989-721-369
32	60.5	16.9	447	10	US-09-992-598-369
33	60.5	16.9	447	10	US-09-992-598-369
34	60.5	16.9	447	10	US-09-989-293A-369
35	60.5	16.9	447	10	US-09-989-735-369
36	60.5	16.9	447	10	US-09-990-444-369
37	60.5	16.9	447	10	US-09-991-181-369
38	60.5	16.9	447	10	US-09-989-730-369
39	60.5	16.9	447	10	US-09-990-436-369
40	60.5	16.9	447	10	US-09-993-687-369
41	60.5	16.9	447	11	US-09-989-734-369
42	60.5	16.9	447	11	US-09-997-653-369
43	60.5	16.9	447	11	US-09-993-667-369
44	60.5	16.9	447	11	US-09-997-428-369
45	60.5	16.9	447	11	US-09-997-666-369

ALIGNMENTS

RESULT 1  
US-09-289-346A-5  
; Sequence 5, Application US/09289346A  
; Patent No. US2002013867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (47)..(49)  
; OTHER INFORMATION: Description of Artificial Sequence. Fragment of  
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine  
; OTHER INFORMATION: replacements (EKY159->AAA159).  
US-09-289-346A-5

Query Match	100.0%	Score	359	DB	10	Length	70
Best Local Similarity	100.0%	Pred. No.	1.6e-39	Mismatches	0	Indels	0
Matches	70	Conservative	0	0	Gaps	0	0
QY	1	TLVWGFEQVDRSARGGCT	NDAAAEALNASSKEBALQIIRKIPAAALFQFHNLNSL	60			
Db	1	TLVWGFEQVDRSARGGCT	NDAAAEALNASSKEBALQIIRKIPAAALFQFHNLNSL	60			
QY	61	DRIFDKTPEP	70				

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Db          61 DRIFDKTPEP 70
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110 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 169

RESULT 4
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9

Query Match      93.3%; Score 335; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 2.2e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy          1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
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Db          1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60

Qy          61 DRIFDKTPEP 70
|||||
Db          61 DRIFDKTPEP 70

RESULT 5
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12

Query Match      92.5%; Score 332; DB 10; Length 70;

Db          61 DRIFDKTPEP 70
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110 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 169

RESULT 2
US-09-289-346A-1
; Sequence 1, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-1

Query Match      95.5%; Score 343; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 2e-37; 3; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy          1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
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Db          1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60

Qy          61 DRIFDKTPEP 70
|||||
Db          61 DRIFDKTPEP 70

RESULT 3
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11

Query Match      95.5%; Score 343; DB 10; Length 356;
Best Local Similarity 95.7%; Pred. No. 1.7e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy          1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
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```
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->AA118).
US-09-289-346A-8

Query Match          91.6%; Score 329; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFQFHNLSNL 60
   |||||
Db 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFQFHNLSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 6
US-09-289-346A-16
; Sequence 16, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-16

Query Match          92.2%; Score 331; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 7.5e-36;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFQFHNLSNL 60
   |||||
Db 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFQFHNLSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 7
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE: VARIANT
; NAME/KEY: (7)..(8)
; LOCATION: (7)..(8)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
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; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->AA118).
US-09-289-346A-8

Query Match          91.6%; Score 329; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFQFHNLSNL 60
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Db 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFQFHNLSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 8
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14

Query Match          91.6%; Score 329; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFQFHNLSNL 60
   |||||
Db 1 TLVWGEFQVDRSARGGCQTSDNDAALNASSKEALQIIREKIPAAALFQFHNLSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 9
US-09-289-346A-2
; Sequence 2, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
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; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAAA125).
US-09-289-346A-2

Query Match          91.4%; Score 328; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.9e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 60
Db 1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLQFHNLNSNL 60

QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAA136->LLLL136).
US-09-289-346A-10

Query Match          91.4%; Score 328; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.9e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 60
Db 1 TLVWGEFQVDRSARGCGCQTSNDLLLEALNASSKEEALQIIREKIPKYLQFHNLNSNL 60

QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
```

```
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-13

Query Match          91.1%; Score 327; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 2.5e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 60
Db 1 TLVWGEFQVDRSARGCGCQTSAAAAAEALNASSKEEALQIIREKIPKYLQFHNLNSNL 60

QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-4
; Sequence 4, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (42)..(44)
; OTHER INFORMATION: Description of Artificial sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REK154->AAA154).
US-09-289-346A-4

Query Match          90.5%; Score 325; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 4.6e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLNSNL 60
Db 1 TLVWGEFQVDRSARGCGCQTSNDAAAEALNASSKEEALQIIRAAAIPKYLQFHNLNSNL 60

QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
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; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match      90.5%; Score 325; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. NO. 4.6e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPAAALFQPHNLNSNL 60
Db 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSAAALQIIREKIPKYLQFPHNLNSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 14
US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (59)..(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDRI172->ALAA172).
US-09-289-346A-7

Query Match      89.4%; Score 321; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. NO. 1.5e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPAAALFQPHNLNSNL 60
Db 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYLQFPHNLNSAL 60
QY 61 DRIFDKTPEP 70
Db 61 AAFIDKTPEP 70

```

```

RESULT 15
US-09-289-346A-6
; Sequence 6, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (52)..(55)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (QFHN165->APAA165).
US-09-289-346A-6

Query Match      88.9%; Score 319; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. NO. 2.8e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPAAALFQPHNLNSNL 60
Db 1 TLVWGEFQV DGRSARGGCQTSDNDAAEALNASSKEEALQIIREKIPKYLQFPHNLNSNL 60
QY 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70

Search completed: December 23, 2003, 09:43:29
Job time : 76 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds  
(without alignments)  
673.181 Million cell updates/sec

Title: US-09-289-346B-5  
Perfect score: 359  
Sequence: 1 TLVWGFQVDRSARGGQCT.....FOFHNLNSNLDRIFDKTPPEP 70  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	343	95.5	352	1 QOCVLI	Al1 protein - toma
2	247	68.8	361	1 QOCVPT	Al1 protein - toma
3	243	67.7	358	2 S07594	hypothetical prote
4	232	64.6	362	1 JQ1887	Al1 protein - toma
5	226	63.0	359	2 S39211	gene Cl protein -
6	224	62.4	349	2 JQ2300	replicase - pepper
7	224	62.4	349	2 S31875	Al1 protein - pepp
8	219	61.0	359	2 S22593	hypothetical prote
9	216	60.2	351	2 JQ2327	Al1 protein - Indi
10	216	60.2	358	1 JQ1870	Al1 protein - toma
11	215	59.9	355	1 QOCVW1	AV1 protein - abut
12	213	59.3	359	2 S39235	gene Cl protein -
13	212	59.1	385	2 S28360	Al1 protein - beet
14	209	58.2	360	2 S59885	replication-associ
15	203	56.5	357	1 QOCVC1	Al1 protein - toma
16	134	37.3	131	2 S45059	AC1 protein (clone
17	118	32.9	347	1 QOCVW1	Al1 protein - squa
18	85	18.1	587	2 JCL1419	Fc gamma (IgG) rec
19	63.5	17.7	1033	2 E97700	hypothetical prote
20	63.5	17.7	1713	2 A55347	adhesive ligand ep
21	62.5	17.4	642	2 D90558	topoisomerase iv s
22	62	17.3	160	2 G82060	hypothetical prote
23	62	17.3	308	2 E86840	protein maturation
24	61.5	17.1	300	2 G89582	protein maturation
25	61.5	17.1	538	2 AD0285	probable periplasm
26	61	17.0	631	2 S36505	E1 protein - human
27	61	17.0	840	2 T36175	probable large ATP
28	60.5	16.9	338	2 AG3582	iron(III)-binding
29	60.5	16.9	429	2 A44384	GTP-binding regula

30 60.5 16.9 435 2 E59096 hypothetical prote  
31 60.5 16.9 447 2 T12544 hypothetical prote  
32 60.5 16.9 1070 1 A54600 1-phosphatidylinos  
33 60 16.7 397 2 B71078 probable NADH oxid  
34 60 16.7 714 2 C95382 probable ferrichro  
35 59.5 16.6 706 2 H71707 hypothetical prote  
36 59.5 16.6 1053 2 T06483 probable ubiquitin  
37 59.5 16.6 1610 2 A46227 voltage-dependent  
38 59.5 16.6 1646 2 JH0422 voltage-dependent  
39 59.5 16.6 2137 2 T05244 hypothetical prote  
40 59.5 16.6 2161 2 JH0564 hypothetical prote  
41 59.5 16.6 2181 2 A38198 calcium channel al  
42 59.5 16.6 2203 2 T42742 voltage-dependent  
43 59 16.4 351 2 AF2626 hypothetical prote  
44 59 16.4 351 2 E97408 fbpa (AR006039) [i  
45 59 16.4 451 2 S26839 retrovirus-related

#### ALIGNMENTS

##### RESULT 1

QOCVLI  
Al1 protein - tomato golden mosaic virus  
C:Species: tomato golden mosaic virus  
A:Note: host Nicotiana sp. (tobacco)  
C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Apr-1994  
C:Accession: A04170  
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.  
EMBO J. 3, 2197-2205, 1984  
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomato golden mosaic virus  
A:Reference number: A04163  
A:Accession: A04170  
A:Molecule type: DNA  
A:Residues: 1-352 <HAM>  
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A and DNA B.  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 95.5%; Score 343; DB 1; Length 352;  
Best Local Similarity 95.7%; Pred. NO. 1.6e-31;  
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TLVWGFQVDRSARGGQCTSDNDAAAEALNASSKEEALQIIREKIPAAALFOFHNLNSNL 60  
DB 111 TLVWGFQVDRSARGGQCTSDNDAAAEALNASSKEEALQIIREKIPAAALFOFHNLNSNL 170  
QY 61 DRIFDKTPPEP 70  
DB 171 DRIFDKTPPEP 180

##### RESULT 2

QOCVPT  
Al1 protein - potato yellow mosaic virus (isolate Venezuela)  
C:Species: potato yellow mosaic virus  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jun-2000  
C:Accession: JU0364  
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.  
J. Gen. Virol. 72, 1515-1520, 1991  
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yellow mosaic virus  
A:Reference number: JU0362; MUID:91311403; PMID:1856690  
A:Accession: JU0364  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-361 <COU>  
A:Cross-references: GB:D00940; NID:G222458; PIDN:BAA00782.1; PID:G222459  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus Al1 protein



Query Match 60.2%; Score 216; DB 2; Length 351;  
Best Local Similarity 62.7%; Pred. No. 5.4e-17;  
Matches 42; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

S39235  
gene C1 protein - tomato yellow leaf curl virus  
C:Species: tomato yellow leaf curl virus  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Sep-1997  
C:Accession: S39235  
R:Crepi, S.; Noris, E.; Vaira, A.; Bosco, D.; Accotto, G.  
submitted to the EMBL Data Library, December 1993  
A:Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.  
A:Reference number: S39233  
A:Accession: S39235  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-359 <CRE>  
A:Cross-references: EMBL:Z28390; NID:g1041671; PID:gl334964  
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.3%; Score 213; DB 2; Length 359;  
Best Local Similarity 56.5%; Pred. No. 1.2e-16;  
Matches 39; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 2 LVNGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQPHNLSNLD 61  
Db 111 LEWGTFTIDGRSARGGCGTANDAYAKAINRSKSEALDVIKQLAPRDYVLHFHNISNLD 170

Qy 62 RIFDKTPEP 70  
Db 171 KVQVPPAP 179

RESULT 13  
S28360  
AL1 protein - beet curly top virus  
C:Species: beet curly top virus  
C>Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Sep-1999  
C:Accession: S28360  
R:Stanley, J.; Markham, P.G.; Callis, R.J.; Pinner, M.S.  
EMBO J. 5, 1761-1767, 1986  
A:Title: The nucleotide sequence of an infectious clone of the geminivirus beet curly top  
A:Reference number: S28360  
A:Accession: S28360  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-385 <STA>  
A:Cross-references: GB:M24597; EMBL:X04144; NID:g210678; PIDN:AAA42751.1; PID:g210679  
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.1%; Score 212; DB 2; Length 385;  
Best Local Similarity 55.7%; Pred. No. 1.7e-16;  
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQPHNLSNLD 60  
Db 137 TIEWGEFQIDGRSARGGCGTANDSVAKALNATSLDQALQILKEQPKDYFLQHHNLNNA 196

Qy 61 DRIFDKTPEP 70  
Db 197 QKIFQRPDP 206

RESULT 14  
S59885  
replication-associated protein C1 - tomato yellow leaf curl virus  
C:Species: tomato yellow leaf curl virus  
C>Date: 14-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 20-Sep-1999  
C:Accession: S59885  
R:Hong, Y.; Harrison, B.D.  
submitted to the EMBL Data Library, February 1995  
A:Description: Nucleotide sequences from tomato leaf curl viruses from different countries  
d geminiviruses.  
A:Reference number: S58346  
A:Accession: S59885  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-360 <HON>  
A:Cross-references: EMBL:Z48182; NID:g944838; PIDN:CAA88229.1; PID:g974211  
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 58.2%; Score 209; DB 2; Length 360;  
Best Local Similarity 62.1%; Pred. No. 3.5e-16;  
Matches 41; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 4 WGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQPHNLSNLDRI 63  
Db 113 FGVFQIDGRSARGGCGQSANDAYAEALNSGSKAAALDIILREKAPKDFVLQPHNLSNLDRI 172

Qy 64 FDKTPE 69  
Db 173 FTPEAE 178

RESULT 15  
QQCVCI  
AL1 protein - tomato yellow leaf curl virus  
N:Alternate names: C1 protein  
C:Species: tomato yellow leaf curl virus  
C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
C:Accession: D40779  
R:Navot, N.; Pichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.  
Virology 185, 151-161, 1991  
A:Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single  
A:Reference number: A40779; MUID:92024070; PMID:1926771  
A:Accession: D40779  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-357 <NAV>  
A:Cross-references: GB:X15656; NID:g62204; PIDN:CAA33688.1; PID:g62207  
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 56.5%; Score 203; DB 1; Length 357;  
Best Local Similarity 65.6%; Pred. No. 1.7e-15;  
Matches 40; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 4 WGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPAAALFQPHNLSNLDRI 63  
Db 111 FGVSQIDGRSARGGCGQSANDAYAEALNSGSKSEALNLIKKEAPKDYILOPHNLSNLDRI 170

Qy 64 F 64  
Db 171 F 171

Search completed: December 23, 2003, 09:05:21  
Job time : 11 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.7778 Seconds  
(without alignments)  
569.747 Million cell updates/sec

Title: US-09-289-346b-5  
Perfect score: 359  
Sequence: 1 TLWGEFQVDRSARGGCQT.....FQFHLNSLDRFDKTPPEP 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	343	95.5	352	1 VAL1_TGMV	P03567 tomato gold
2	247	68.8	361	1 VAL1_PYMV	P27258 potato yell
3	243	67.7	358	1 VAL1_CLVK	P14982 cassava lat
4	243	67.7	358	1 VAL1_CLVN	P14972 cassava lat
5	232	64.6	362	1 VAL1_TYLCU	P36279 tomato yell
6	226	63.0	359	1 VAL1_TYLCU	P38609 tomato yell
7	224	62.4	349	1 VAL1_PHVU	Q06923 pepper huas
8	219	61.0	359	1 VAL1_TYLCM	P27260 tomato yell
9	216	60.2	353	1 VAL1_BGMV	P05175 bean golden
10	216	60.2	361	1 VAL1_TMOV	P06657 tomato mott
11	215	59.9	355	1 VAL1_ABMVW	P21947 abutilon mo
12	212	59.1	358	1 VAL1_BCTV	P14991 beet curly
13	203	56.5	357	1 VAL1_TYLCV	P27259 tomato yell
14	118	32.9	347	1 VAL1_SLVC	P29048 squash leaf
15	65	18.1	630	1 VE1_HPV66	Q80957 human papil
16	64.5	18.0	298	1 OLG2_CHICK	Q90xb3 gallus gall
17	63.5	17.7	298	1 LNA3_HUMAN	Q16787 homo sapien
18	62.5	17.4	428	1 GBAL_CANAL	P28868 candida alb
19	61.5	17.1	476	1 DGRE_HUMAN	Q96df8 homo sapien
20	61.5	17.1	479	1 DGRE_MOUSE	Q70279 mus musculus
21	61	17.0	631	1 VE1_HPV30	Q05112 human papil
22	60.5	16.9	447	1 TBL2_HUMAN	Q9v4p3 homo sapien
23	60.5	16.9	1070	1 P11B_HUMAN	P42338 homo sapien
24	59.5	16.6	706	1 Y006_RICPR	Q9zed6 rickettsia
25	59.5	16.6	1053	1 UBA3_WHEAT	P31252 triticum ae
26	59.5	16.6	1610	1 CCAD_MESAU	Q99244 mesocricetu
27	59.5	16.6	2161	1 CCAD_HUMAN	Q01668 homo sapien
28	59.5	16.6	2203	1 CCAD_RAT	P27732 rattus norv
29	59	16.4	703	1 GYS2_RAT	P17625 rattus norv
30	59	16.4	1852	1 CCAS_CYPCA	P22316 cyprinus ca
31	58	16.2	387	1 YAPF_RHTSN	P55615 rhizobium s
32	58	16.2	1127	1 Y855_TREPA	O83827 treponema p
33	58	16.2	1608	1 HLVA_SERMA	P15320 serratia ma

## ALIGNMENTS

### RESULT 1

VAL1\_TGMV STANDARD; PRT; 352 AA.  
AC P03567;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE AL1 protein.  
GN AC1.  
OS Tomato golden mosaic virus (TGMV).  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=10831;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;  
RT "Complete nucleotide sequence of the infectious cloned DNA components of tomato golden mosaic virus: potential coding regions and regulatory sequences.";  
RL EMBL J. 3:2197-2205(1984).  
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).  
EMBL; K02029; -; NOT\_ANNOTATED\_CDS.  
PIR; A04170; QQCVL1.  
InterPro; IPR001191; Gemini\_AL1.  
Pfam; PF00799; Gemini\_AL1; 1.  
PRINTS; PR00227; GEMCOATAL1.  
ProDom; PD000736; Gemini\_AL1; 1.  
ATP-binding.  
NP\_BIND 223 230 ATP (POTENTIAL).  
SQ SEQUENCE 352 AA; 40332 MW; C33C938E9644B44 CRC64;  
Query Match 95.5%; Score 343; DB 1; Length 352;  
Best Local Similarity 95.7%; Pred. No. 6.1e-32;  
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TLWGEFQVDRSARGGCQTSDNAAALNASSKEEALQIIREKIPAAALQFHLNSNL 60  
DB 111 TLWGEFQVDRSARGGCQTSDNAAALNASSKEEALQIIREKIPKYLFPFHLNSNL 170  
QY 61 DRFDKTPPEP 70  
DB 171 DRFDKTPPEP 180  
RESULT 2  
VAL1\_PYMV STANDARD; PRT; 361 AA.  
AC P27258;

```
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
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CC
CC -----
DR EMBL; D00940; BAA00782.1; -.
DR PIR; J00364; QOCVPT.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;

Query Match
Best Local Similarity 68.8%; Score 247; DB 1; Length 361;
Matches 47; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGQTSNDAAAEALNASSKEALQIIREKIPAAALFQPHNLSNL 60
Db 110 TIWGLFQIDGRSARGCGQTVNDAAAEALNASSKEALQIIREKIPAAALFQPHNLSNL 169
QY 61 DRIFDKTPE 69
Db 170 DRIFDKAPE 178

RESULT 3
VALI_CLVK STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN ACl.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RX Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA."
RL Nature 301:260-262(1983).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
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CC
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CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753BE92D69 CRC64;

Query Match
Best Local Similarity 67.7%; Score 243; DB 1; Length 358;
Matches 45; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGQTSNDAAAEALNASSKEALQIIREKIPAAALFQPHNLSNL 60
Db 109 TIWGLFQIDGRSARGCGQTSNDAAAEALNASSKEALQIIREKIPAAALFQPHNLSNL 168
QY 61 DRIFDKTPE 70
Db 169 DRIFQEPAP 178

RESULT 4
VALI_CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN ACl.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308931;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain)."
RL Nucleic Acids Res 18:197-198(1990).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
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CC
CC -----
DR EMBL; X17095; CAA34953.1; -.
DR PIR; S07594; S07594.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16BB0CB2D5E2C CRC64;

Query Match
Best Local Similarity 67.7%; Score 243; DB 1; Length 358;
Matches 45; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGQTSNDAAAEALNASSKEALQIIREKIPAAALFQPHNLSNL 60
Db 109 TIWGLFQIDGRSARGCGQTSNDAAAEALNASSKEALQIIREKIPAAALFQPHNLSNL 168
QY 61 DRIFDKTPE 70
Db 169 DRIFQEPAP 178
```

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-----
CC EMBL; Z25751; CAA81026.1; -.
DR PIR; S39211; S39211.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3EC CRC64;

Query Match 63.0%; Score 226; DB 1; Length 359;
Best Local Similarity 60.9%; Pred. No. 1.7e-18;
Matches 42; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 2 LVWGEFQVDRSARGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQPHNLNSLD 61
Db 111 LEWGTFFQIDGRSARGGQQTANDAYAKAINAGSKSEALDVIKELAPRDVILHFFHNSLD 170

QY 62 RIFDKTPEP 70
Db 171 RVFQVPPAP 179

RESULT 7
VAL1 PHUV STANDARD; PRT; 349 AA.
ID VAL1 PHUV
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AL1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
RT comparison with bipartite geminiviruses.";
RL J. Gen. Virol. 74:2225-2231(1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC EMBL; X70418; CAA49856.1; -.
DR PIR; JQ2300; JQ2300.
DR PIR; S31875; S31875.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 39722 MW; D5F4E76CD56370F4 CRC64;

Query Match 62.4%; Score 224; DB 1; Length 349;
Best Local Similarity 61.4%; Pred. No. 2.7e-18;
Matches 43; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQPHNLNSLD 60
Db 110 TVWGEFQIDGRSARGGQTSNDTAKALNSAAEALQIIEKEQPHFFLOFHNVSNA 169

-----
RESULT 5
VAL1 TYLCU STANDARD; PRT; 362 AA.
ID VAL1 TYLCU
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36447;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93139778; PubMed=8423446;
RA Dry I.B., Rigden J.E., Krake L.R., Mullineaux P.M., Rezaian M.A.;
RT "Nucleotide sequence and genome organization of tomato leaf curl
RT geminivirus.";
RL J. Gen. Virol. 74:147-151(1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR PIR; JQ1887; JQ1887.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;

Query Match 64.6%; Score 232; DB 1; Length 362;
Best Local Similarity 55.3%; Pred. No. 3.4e-19;
Matches 47; Conservative 8; Mismatches 14; Indels 16; Gaps 1;

QY 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQPHNLNSLD 60
Db 110 TLEWGEFQIDGRSARGGQTSANDAYAKALNTGSKSEALNVRELAPKDYVLQPHNLNSLD 169

QY 61 DRI-----FDKTPK 69
Db 170 DRIPTPLEVYVSPFLSSFDVRPE 194

RESULT 6
VAL1 TYLCU STANDARD; PRT; 359 AA.
ID VAL1 TYLCU
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Noris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
RT from the west Mediterranean basin: the nucleotide sequence of an
RT infectious clone from Spain.";
RL Arch. Virol. 135:165-170(1994).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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QY 61 DRIFDKTPEP 70
Db 170 NRIFQTPPEP 179

RESULT 8
VAL1_TYLCM STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP MEDLINE=92107660; PubMed=1840676;
RA Khayr-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
RA Gronenborn B.;
RA "Tomato yellow leaf curl virus from Sardinia is a
RT whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
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CC
CC EMBL; M10070; AAA46318.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
KW NP BIND 222 229 ATP (POTENTIAL).
FT SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;
SQ
Query Match 60.2%; Score 216; DB 1; Length 353;
Best Local Similarity 60.0%; Pred. No. 2.3e-17;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRGARGCGTSDNAAAEALNAGSKKEALQIIREKIPAAALFQFHNLNSNL 60
Db 110 TLVWGFQVDRGARGCGTSDNAAAEALNAGSKKEALQIIREKIPAAALFQFHNLNSNL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFFKVPEP 179

RESULT 10
VAL1_TMOV STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AL1.
OS Tomato mottle virus (isolate Florida) (TMOV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36449;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93107856; PubMed=1469361;
RA Abouzid A.M., Polston J.E., Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida.";
RL J. Gen. Virol. 73:3225-3229(1992).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
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CC
CC EMBL; L14460; AAC32414.1; -.
DR PIR; JQ1870; JQ1870.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.

QY 2 LVWGFQVDRGARGCGTSDNAAAEALNAGSKKEALQIIREKIPAAALFQFHNLNSNL 61
Db 111 LVWGFQVDRGARGCGTSDNAAAEALNAGSKKEALQIIREKIPAAALFQFHNLNSNL 170
QY 62 RIFDKTPEP 70
Db 171 KVQFVPPAP 179

RESULT 9
VAL1_BGMV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE AL1 protein (40.2 kDa protein).
GN AC1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
```



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DR EMBL; X15656; CAA33688.1; -.
DR FIR; D40779; QOCVCL; Gemini_AL1.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 219 226 ATP (POTENTIAL).
SQ SEQUENCE 357 AA; 40678 MW; 939AB681A3B2A7 CRC64;

Query Match 56.5%; Score 203; DB 1; Length 357;
Best Local Similarity 65.6%; Pred. No. 7.1e-16;
Matches 40; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 4 WGFQVDGRSARGCGTSDNDAAEALNASSKEALQIIREKIPAAALFOFHNLNSLDRIF 63
DB 111 FGVSQIDGRSARGGQSQANDAYAEALNASSKEALNLIKERKPKDYILQFHNLSSLDRIF 170

QY 64 F 64
DB 171 F 171

RESULT 14
VAL1 SLCV STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE A11 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G., Laxdins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype."
RL Virology 180:58-69(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC -----
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CC -----
CC EMBL; M38183; AAC32410.1; ALT_INIT.
CC FIR; C36785; QOCVSL.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATL1.
CC ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDABDDDEL22110E CRC64;

Query Match 32.9%; Score 118; DB 1; Length 347;
Best Local Similarity 37.9%; Pred. No. 3.9e-06;
Matches 25; Conservative 12; Mismatches 25; Indels 4; Gaps 1;

QY 5 GEFQVDGRSARGCGTSDNDAAEALNASSKEALQIIREKIPAAALFOFHNLNSLDRIF 64
DB 116 GQYKVSQ-----GSKSNKDDVYHNAYNAGSAGEALDIIRAGDPKTFIVNHNLLANVERLF 171

QY 65 DKTPRP 70
DB 172 QKPPRP 177
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RESULT 15
VE1_HPV66 STANDARD; PRT; 630 AA.
ID VE1_HPV66
AC Q80957;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Replication protein E1.
GN E1.
OS Human papillomavirus type 66.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=371119;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -----
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CC -----
CC EMBL; U31794; AAA79501.1; -.
CC InterPro; IPR001177; Papillom_E1.
CC Pfam; PF00519; E1; 1.
CC Pfam; PF00524; E1_N; 1.
KW Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
KW Nuclear protein.
FT NP_BIND 458 465 ATP (POTENTIAL).
SQ SEQUENCE 630 AA; 72065 MW; 22DDDA5934F7291B CRC64;

Query Match 18.1%; Score 65; DB 1; Length 630;
Best Local Similarity 25.5%; Pred. No. 9.3;
Matches 13; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 19 QTSNDAAAEALNASSKEALQIIREKIPAAALFOFHNLNSLDRIFDKTPE 69
DB 269 KTIYKSLSSILNVQEQMLIQPKLRSPAVALYFYKTAMSNISEVYGETPE 319

Search completed: December 23, 2003, 08:57:38
Job time : 5.77778 secs
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 25.3333 Seconds  
(without alignments)  
713.040 Million cell updates/sec

Title: US-09-289-346B-5  
Perfect score: 359  
Sequence: 1 TLVWGEFQDGRSARGGQCT.....FOFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum Match 100%  
Listing first 45 summaries  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	298	83.0	351	Q91R10	Q91R10 tomato seve
2	296	82.5	352	Q9E000	Q9E000 tomato rugo
3	288	80.2	232	Q8QPV3	Q8QPV3 tomato chlo
4	287	79.9	226	Q9WHF6	Q9WHF6 tomato mild
5	277	77.2	361	Q67574	Q67574 bean golden
6	275	76.6	225	Q9QDB1	Q9QDB1 cowpea gold
7	275	76.6	226	Q09727	Q09727 leonurus mo
8	271	75.5	185	Q98693	Q98693 sida golden
9	271	75.5	314	Q9ELT8	Q9ELT8 sweet potat
10	271	75.5	364	Q9QS55	Q9QS55 sweet potat
11	268	74.7	235	Q9QPU4	Q9QPU4 tomato infe
12	267	74.4	208	Q8JLY3	Q8JLY3 potato yell
13	267	74.4	289	Q8JLY5	Q8JLY5 potato yell
14	264	73.5	149	P88975	P88975 macroptiliu
15	264	73.5	190	Q9Z089	Q9Z089 tobacco lea
16	264	73.5	190	Q9Z084	Q9Z084 tobacco lea

17	264	73.5	233	12	Q9YLA4	Q9YLA4 macroptiliu
18	263	73.3	190	12	Q9W827	Q9W827 tobacco lea
19	263	73.3	208	12	Q9Z0C4	Q9Z0C4 tobacco lea
20	263	73.3	359	12	Q91M88	Q91M88 tobacco lea
21	263	73.3	359	12	Q8TV88	Q8TV88 tomato curl
22	263	73.3	361	12	Q8TMJ4	Q8TMJ4 potato yell
23	261	72.7	208	12	Q9Z0C0	Q9Z0C0 tobacco lea
24	261	72.7	208	12	Q9Z0B8	Q9Z0B8 tobacco lea
25	259	72.1	208	12	Q9Z0B6	Q9Z0B6 tobacco lea
26	259	72.1	361	12	Q8QVH0	Q8QVH0 ageratum en
27	258	71.9	203	12	Q9Z083	Q9Z083 tobacco lea
28	258	71.9	234	12	Q39180	Q39180 geminivirid
29	257	71.6	360	12	Q8QMH4	Q8QMH4 sida mottie
30	256	71.3	223	12	Q8QPU7	Q8QPU7 tomato seve
31	251	69.9	208	12	Q9Z0A0	Q9Z0A0 tobacco lea
32	251	69.9	363	12	Q72719	Q72719 cotton leaf
33	251	69.9	363	12	Q72705	Q72705 cotton leaf
34	250	68.6	190	12	Q9Z086	Q9Z086 tobacco lea
35	250	69.6	208	12	Q9Z0C6	Q9Z0C6 tobacco lea
36	249	69.4	349	12	Q88888	Q88888 tomato pseu
37	249	69.4	363	12	Q73577	Q73577 cotton leaf
38	249	69.4	364	12	Q8V524	Q8V524 ipomoea lea
39	248	69.1	359	12	Q91B86	Q91B86 ageratum ye
40	248	69.1	360	12	Q9DX10	Q9DX10 ageratum ye
41	247	68.8	348	12	Q911W5	Q911W5 macroptiliu
42	246	68.5	190	12	Q9Z0A7	Q9Z0A7 tobacco lea
43	246	68.5	362	12	Q8V016	Q8V016 cotton leaf
44	246	68.5	362	12	Q8V018	Q8V018 cotton leaf
45	246	68.5	362	12	Q8V618	Q8V618 cotton leaf

ALIGNMENTS

RESULT 1  
Q91R10 PRELIMINARY; PRT; 351 AA.  
ID Q91R10  
AC Q91R10;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Rep protein.  
GN AC1.  
OS Tomato severe rugose virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=158463;  
RN [1]\_\_TaxID=158463;  
RP SEQUENCE FROM N.A.  
RC STRAIN=Minas Gerais;  
RA Rezende W.L., Goulart L.R., Parreira K.S., Figueiredo J.E.F.;  
RT "The full-length DNA-A nucleotide sequence of a novel tomato-infecting  
RT begomovirus, Tomato severe rugose virus, in Brazil."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY029750; RAKS0357.1; -  
DR InterPro; IPR001191; Geminivirus.  
DR Pfam; PF00799; Geminivirus.  
DR PRINTS; PR00227; GEMCOATALI.  
DR ProDom; PD000736; Geminivirus.  
SQ SEQUENCE 351 AA; 40122 MW; 87F937A4F873B6CF CRC64;

Query Match 83.0%; Score 298; DB 12; Length 351;  
Best Local Similarity 80.0%; Pred. No. 1.4e-26;  
Matches 56; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY	1	TLVWGEFQDGRSARGGQCTNSNDAAEALNSKKEALQITREKIPAAALFOFHNLNSL 60
Db	111	TLVWGEFQDGRSARGGQCTNSNDAAEALNSKKEALQITREKIPAAALFOFHNLNSL 170
QY	61	DRIFDKTPEP 70
Db	171	DRIFDKTPEP 180

QY 1 TLVWGEFQVDGRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60

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RT hybridization probes and aspects of bean golden mosaic in Brazil.";
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus.";
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M88686; AAA46312.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 77.2%; Score 277; DB 12; Length 361;
Best Local Similarity 77.6%; Pred. No. 4.2e-24;
Matches 52; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 WGEFQVDGRSARGGCOTSNDAAEALNASSKEKALQIIREKIPAAALFQPHNLSNLDRI 63
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
113 WGHFQVDGRSARGGCQTANDAAEALNASSKEAMQIIEKLPKFLFQYHNLSSNLDRI 172

QY 64 FDKTPEP 70
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
173 FTKAPDP 179

RESULT 6
Q9QDB1 PRELIMINARY; PRT; 225 AA.
ID Q9QDB1;
AC Q9QDB1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Cowpea golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGMV-BR;
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RT Brazil.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF188708; AAF06318.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 225
SQ SEQUENCE 225 AA; 25766 MW; 1089CB6BD8D15B5D CRC64;

Query Match 76.8%; Score 275; DB 12; Length 225;
Best Local Similarity 77.6%; Pred. No. 4.1e-24;
Matches 52; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 4 WGEFQVDGRSARGGCOTSNDAAEALNASSKEKALQIIREKIPAAALFQPHNLSNLDRI 63
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
113 WGHFQVDGRSARGGCQTINDAAEALNASSKEAMQIIEKLPKFLFQYHNLSSNLDRI 172

QY 64 FDKTPEP 70
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
173 FKKPPEP 179

RESULT 7
O09727 PRELIMINARY; PRT; 226 AA.
ID O09727
AC O09727;

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DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN REP.
OS Leonurus mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=58177;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LemV- Brazil 1;
RA Faria J.C., Maxwell D.P.;
RT "Variability in geminivirus associated with Phaseolus vulgaris in
RT Brazil.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U92532; AAB51157.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 226
SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;

Query Match 76.6%; Score 275; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 4.1e-24;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGRSARGGCOTSNDAAEALNASSKEKALQIIREKIPAAALFQPHNLSN 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
111 TVWGEFQVDGRSARGGCQTVDAAEALNAPDKRTALQIIEKLPKFLFQYHNLSSN 170

QY 61 DRIFDKTPEP 70
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
171 DRIFAKAPEP 180

RESULT 8
Q98693 PRELIMINARY; PRT; 185 AA.
ID Q98693;
AC Q98693;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Jamaica;
RA Roye M.E., McLaughlin W.A., Nakhla N.K., Maxwell D.P.;
RT "Genetic Diversity among geminiviruses associated with the weed
RT species Sida spp, Macroptilium lathyroides, and Wissadula amplissima
RT from Jamaica.";
RL Plant Dis. 81:1251-1258(1997).
DR EMBL; U67926; AAB37865.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 185
SQ SEQUENCE 185 AA; 20975 MW; 3913850A025A5EE1 CRC64;

Query Match 75.5%; Score 271; DB 12; Length 185;
Best Local Similarity 71.4%; Pred. No. 9.6e-24;
Matches 50; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGRSARGGCOTSNDAAEALNASSKEKALQIIREKIPAAALFQPHNLSN 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
89 TIWGVFQVDGRSARGGCQTANDAAEALNSGKEDALKIIEKLPKFLFQYHNLSSNI 148

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QY 61 DRIPDKTPEP 70
Db 149 DRIFSKPPEP 158

RESULT 9
Q9ELT8 PRELIMINARY; PRT; 314 AA.
AC Q9ELT8, 2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Replication associated protein.
GN ACI.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF298227; AAG01006.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 75.5%; Score 271; DB 12; Length 314;
Best Local Similarity 79.4%; Pred. No. 1.8e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60
Db 110 TITWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 169

QY 61 DRIPDKTPEP 68
Db 170 DRIFSPPP 177

RESULT 10
Q9QSS5 PRELIMINARY; PRT; 364 AA.
AC Q9QSS5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Replication initiation protein ACI.
GN ACI.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RL virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0(1999).
DR EMBL; AF104036; AAD47173.1; -.
DR InterPro; IPR001191; Gemini_AL1.

Query Match 75.5%; Score 271; DB 12; Length 314;
Best Local Similarity 79.4%; Pred. No. 1.8e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60
Db 110 TITWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 169

QY 61 DRIPDKTPEP 68
Db 170 DRIFSPPP 177

RESULT 11
Q8QPU4 PRELIMINARY; PRT; 235 AA.
AC Q8QPU4;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN ACI.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RA Ribeiro S.G., Ambrozewicz L.P., de Avila A.C., Calegario R.F.,
RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049208; AAL82833.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 235 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BB0DD9C810 CRC64;

Query Match 74.7%; Score 268; DB 12; Length 235;
Best Local Similarity 74.6%; Pred. No. 2.9e-23;
Matches 50; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 4 WGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 63
Db 113 WGIQFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 172

QY 64 FDKTPEP 70
Db 173 FTKAPDP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN ACI.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

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RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126611; AAM95993.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 208
SQ SEQUENCE 208 AA; 23667 MW; 51211D58FAD690A6 CRC64;

Query Match 74.4%; Score 267; DB 12; Length 208;
Best Local Similarity 71.4%; Pred. No. 3.2e-23;
Matches 50; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEEALQIREKIPAAALFOFHNLSNL 60
Db 110 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEEAMKIIKEKLPKFLFOYHNSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 DRIFWKAPKP 179

RESULT 13
Q8JLY5 PRELIMINARY; PRT; 289 AA.
AC Q8JLY5;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbano C., Polston J.E., Patte C.P., Caruana M.-L.;
RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126610; AAM95993.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 289
SQ SEQUENCE 289 AA; 32971 MW; 4ECF52F4C69C6764 CRC64;

Query Match 74.4%; Score 267; DB 12; Length 289;
Best Local Similarity 71.4%; Pred. No. 4.8e-23;
Matches 50; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEEALQIREKIPAAALFOFHNLSNL 60
Db 110 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEEAMKIIKEKLPKFLFOYHNSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 DRIFWKAPKP 179

RESULT 14
P88975 PRELIMINARY; PRT; 149 AA.
AC P88975;
DT 01-MAY-1997 (TremBLrel. 03, Created)
DT 01-MAY-1997 (TremBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Macropitilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Jamaican;
RA Roye M.E.;
RL Thesis (1996), Biochemistry, University of the West Indies, Jamaica.
DR EMBL; U75278; AAB36919.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 149
SQ SEQUENCE 149 AA; 16785 MW; E4CF5ED4C9CD508 CRC64;

Query Match 73.5%; Score 264; DB 12; Length 149;
Best Local Similarity 70.0%; Pred. No. 4.9e-23;
Matches 49; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEEALQIREKIPAAALFOFHNLSNL 60
Db 52 TIWGLFQIDGRSARGGQTSNDAAAEALNASSKEAMRIYKEKLPKFLFOYHNSNL 111

Qy 61 DRIFDKTPEP 70
Db 112 DRIFWKDPEP 121

RESULT 15
Q9Z089 PRELIMINARY; PRT; 190 AA.
ID Q9Z089
AC Q9Z089;
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Tobacco leaf curl virus C1 and C4 genes, clone YOKOHAMA3-1, partial
DE and complete cds (Fragment).
GN C1.
OS Tobacco leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=67762;
RN [1]
RP SEQUENCE FROM N.A.
RA Ooi K., Ohshita S., Ishii I., Yahara T.;
RT "Molecular phylogeny of geminivirus infecting wild plants in Japan.";
RL J. Plant Res. 110:247-257(1997).
DR EMBL; AB001315; BAA34033.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 190
SQ SEQUENCE 190 AA; 21432 MW; AAC093D1D1610FAD CRC64;

Query Match 73.5%; Score 264; DB 12; Length 190;
Best Local Similarity 62.4%; Pred. No. 6.5e-23;
Matches 53; Conservative 6; Mismatches 10; Indels 16; Gaps 1;

Qy 1 TLVWGEFQVDRSARGGQTSNDAAAEALNASSKEEALQIREKIPAAALFOFHNLSNL 60
Db 85 TLEWGTFOIDGRSARGGQTSNDAAAEALNASSKEALAIKEKLPKDFIFOYHNSNL 144

Qy 61 DRI-----FQKTPPE 69
Db 145 DRIFAPLEVFVCPPTASSFDQVPE 169

Search completed: December 23, 2003, 09:03:35
Job time : 25.3333 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds  
(without alignments)  
340.128 Million cell updates/sec

Title: US-09-289-346B-6  
Perfect score: 357  
Sequence: 1 TLVGEFQVDSRSGGQCT.....FAFALNSLDRIFDKTPEP 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 15872573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*			

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	357	100.0	70	21	AA18682
2	340	95.2	70	21	AA18677
3	340	95.2	356	21	AA18687
4	332	93.0	70	21	AA18685
5	329	92.2	70	21	AA18688
6	328	91.9	70	21	AA18692
7	326	91.3	70	21	AA18684
8	326	91.3	70	21	AA18690
9	325	91.0	70	21	AA18678

10	325	91.0	70	21	AA18686	Mutant peptide der
11	324	90.8	70	21	AA18689	Mutant peptide der
12	322	90.2	70	21	AA18680	Mutant peptide der
13	322	90.2	70	21	AA18691	Mutant peptide der
14	319	89.4	70	21	AA18681	Mutant peptide der
15	318	89.1	70	21	AA18683	Mutant peptide der
16	308	86.3	70	21	AA18679	Mutant peptide der
17	210	58.8	359	17	AA186870	Sardinian tomato y
18	210	58.8	359	17	AA186871	Sardinian tomato y
19	210	58.8	359	17	AA186872	Sardinian tomato y
20	206	57.7	353	18	AA186873	Bean golden mosaic
21	206	57.7	353	18	AA186874	Bean golden mosaic
22	206	57.7	353	18	AA186875	Bean golden mosaic
23	206	57.7	353	18	AA186876	Bean golden mosaic
24	206	57.7	353	18	AA186877	Bean golden mosaic
25	204	57.1	353	18	AA186878	ORF 4 gene product
26	204	57.1	361	18	AA186879	Tomato mottle viru
27	204	57.1	361	18	AA186880	Tomato mottle viru
28	204	57.1	361	18	AA186881	Tomato mottle viru
29	204	57.1	361	18	AA186882	Tomato mottle viru
30	199.5	55.9	50	23	AAO22043	Retinoblastoma-bin
31	197.5	55.3	361	8	AA186883	Product of ORF 4 f
32	192	53.8	362	19	AA186884	Tobacco leaf curl
33	191	53.5	357	18	AA186885	Tomato yellow leaf
34	191	53.5	357	18	AA186886	Tomato yellow leaf
35	191	53.5	357	18	AA186887	Tomato yellow leaf
36	183	51.3	357	18	AA186888	Tomato yellow leaf
37	104	29.1	142	24	ABP58120	Tomato yellow leaf
38	76.5	21.4	665	22	ABP70991	Drosophila melanog
39	76	21.3	857	23	ABP62804	Protein fragment #
40	67	18.8	447	21	AA186889	Human GTPase assoc
41	67	18.8	447	21	AA186890	Human secreted pro
42	67	18.8	447	21	AA186891	Membrane-bound pro
43	67	18.8	447	21	AA186892	Human adult aorta
44	67	18.8	447	22	AA186893	Human PRO polypept
45	67	18.8	447	22	AA186894	Human polypeptide,

ALIGNMENTS

RESULT 1				AA18682
ID	AA18682	standard; peptide; 70 AA.		
XX	AA18682;			
AC	AA18682;			
XX	22-JAN-2001	(first entry)		
DT	22-JAN-2001	(first entry)		
XX	22-JAN-2001	(first entry)		
DE	Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.			
XX	Geminivirus; replication protein; Rep protein; A11; transgenic plant;			
KW	ribosome binding region; resistance; geminivirus infection.			
XX	Synthetic.			
OS	Tomato golden mosaic virus.			
XX	Tomato golden mosaic virus.			
XX	Key	Location/Qualifiers		
FT	Misc-difference 52	/note= "wild type residue replaced with Ala"		
FT	Misc-difference 54	/note= "wild type residue replaced with Ala"		
FT	Misc-difference 55	/note= "wild type residue replaced with Ala"		
XX	WO200054573-A1.			
PN	21-SEP-2000.			
PD	15-MAR-2000; 2000WO-US06759.			
PF	18-MAR-1999; 99US-0125004.			
XX	09-APR-1999; 99US-0289346.			

```

XX PA (UYN-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT
XX PS Claim 53; Page 44-45; 73pp; English.
XX CC
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
XX Query Match 100.0%; Score 357; DB 21; Length 70;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-37;
XX Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLVWGFQVDSARGGCGTSDNDAALNASSKEALQIIREKIPKYLFAFALNSNL 60
DB 1 TLVWGFQVDSARGGCGTSDNDAALNASSKEALQIIREKIPKYLFAFALNSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 2
ID AAB18677 standard; peptide; 70 AA.
XX AC AAB18677;
XX DT 22-JAN-2001 (first entry)
XX DE Peptide fragment from Rep protein of TMV (amino acids 110-179).
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS Tomato golden mosaic virus.
XX PN WO200054573-A1.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000; 2000WO-US06759.
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX PA (UYN-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT
XX PS Disclosure; Page 18; 73pp; English.
XX CC
XX CC The present sequence is derived from a geminivirus replication (Rep)
XX CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
XX CC catalyzes cleavage and ligation of single-stranded DNA, and interacts
XX CC with other viral and host proteins. Mutants of the AL1 protein are used
XX CC to produce transgenic plants. The mutation in AL1 is present in a
XX CC ribosome binding region, and expression of mutant AL1 protein imparts
XX CC increased resistance to geminivirus infection in the plant. Mutant AL1
XX CC proteins are useful for producing plants having increased resistance or
XX CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
XX CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
XX CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
XX CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
XX CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
XX CC beet curly top virus.
XX SQ Sequence 70 AA;
XX Query Match 95.2%; Score 340; DB 21; Length 70;
XX Best Local Similarity 95.7%; Pred. No. 1.8e-35;
XX Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGFQVDSARGGCGTSDNDAALNASSKEALQIIREKIPKYLFAFALNSNL 60
DB 1 TLVWGFQVDSARGGCGTSDNDAALNASSKEALQIIREKIPKYLFAFALNSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 3
ID AAB18687 standard; peptide; 356 AA.
XX AC AAB18687;
XX DT 22-JAN-2001 (first entry)
XX DE Amino acid sequence of a geminivirus replication protein of TMV.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS Tomato golden mosaic virus.
XX FH Key Location/Qualifiers
XX FT Misc-difference 354 /note= "unspecified amino acid"
XX PN WO200054573-A1.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000; 2000WO-US06759.
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX PA (UYN-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT Transgenic plants with increased resistance to geminivirus infection

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comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant ALI protein with a mutation in the Rb binding region

- Disclosure; Page 47-48; 73pp; English.

The present sequence represents a geminivirus replication (Rep) protein, which is also known as ALI. ALI binds double-stranded DNA, catalyses cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the ALI protein are used to produce transgenic plants. The mutation in ALI is present in a ribosome binding region, and expression of mutant ALI protein imparts increased resistance to geminivirus infection in the plant. Mutant ALI proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.

XX Query Match 95.2%; Score 340; DB 21; Length 356;  
XX Best Local Similarity 95.7%; Pred. NO. 1.4e-34;  
XX Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVGFQVDGRSARGGCQTSDNDAAEALNASSKEEALQIREKIPEKYLFAFALNSNL 60  
Db |||||||  
110 TLVGFQVDGRSARGGCQTSDNDAAEALNASSKEEALQIREKIPEKYLFOFFNLNSL 169  
|||

QY 61 DRIFDKTPEP 70  
Db |||||||  
170 DRIFDKTPEP 179  
|||

RESULT 4  
AAB18685  
ID AAB18685 standard; peptide; 70 AA.  
XX AAB18685;  
XX  
XX 22-JAN-2001 (first entry)  
XX Mutant peptide derived from amino acids 110-179 of Rep (ALI) protein.  
XX Geminivirus; replication protein; Rep protein; ALI; transgenic plant;  
XX ribosome binding region; resistance; geminivirus infection.  
XX Synthetic.  
OS Tomato golden mosaic virus.  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 10 /note= "wild type residue replaced with Ala"  
XX  
XX WO200054573-A1.  
PW  
XX  
XX 21-SEP-2000.  
XX  
XX 15-MAR-2000; 2000WO-US06759.  
XX  
XX 18-MAR-1999; 99US-0125004.  
PR 09-APR-1999; 99US-0289346.  
FR  
XX (UYNC-) UNIV NORTH CAROLINA STATE.  
PA  
XX Hanley-Bowdoin L, Orozco BM, Kong L;  
PI WPI; 2000-618851/59.  
XX Transgenic plants with increased resistance to geminivirus infection  
PT comprise a nucleic acid construct containing a nucleic acid sequence

PT	-		encoding a mutant AlI protein with a mutation in the Rb binding region
FT			
XX			
PS	Claim 53; Page 46; 73pp; English.		
XX			
CC	The present sequence represents a mutant peptide, derived from a		
CC	geminivirus replication (Rep) protein, also known as ALI. ALI binds		
CC	double-stranded DNA, catalyses cleavage and ligation of single-stranded		
CC	DNA, and interacts with other viral and host proteins. Mutants of the ALI		
CC	protein are used to produce transgenic plants. The mutation in ALI is		
CC	present in a ribosome binding region, and expression of mutant ALI		
CC	protein imparts increased resistance to geminivirus infection in the		
CC	plant. Mutant ALI proteins are useful for producing plants having		
CC	increased resistance or reduced sensitivity to a geminivirus such as		
CC	tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl		
CC	virus, tomato leaf curl virus, African cassava mosaic virus, Indian		
CC	cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic		
CC	virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper		
CC	virus, cotton leaf curl virus or beet curly top virus.		
XX			
SQ	Sequence      70 AA;		
	Query March                  93.0%; Score 332; DB 21; Length 70;		
	Best Local Similarity    94.3%; Pred. No. 1.9e-34;		
	Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
Qy	1 TLVWGFQVQGRSARGGCQTSDNDAALNASKEEALQITREKIPKYLFAFALNSNL 60		
Db	1 TLVWGFQVAGRSARGGCQTSDNDAALNASKEEALQITREKIPKYLQFFNLNSNL 60		
Qy	61 DRIFDKTPEP 70		
Db	61 DRIFDKTPEP 70		
AC	AAB18688;		
XX	22-JAN-2001 (first entry)		
DE	Mutant peptide derived from amino acids 110-179 of Rep (ALI) protein.		
KW	Geminivirus; replication protein; Rep protein; ALI; transgenic plant;		
XW	ribosome binding region; resistance; geminivirus infection.		
OS	Synthetic.		
OS	Tomato golden mosaic virus.		
XX			
FH	Key                         Location/Qualifiers		
FT	Misc-difference 19                         /note= "wild type residue replaced with Ala"		
FT	Misc-difference 20                         /note= "wild type residue replaced with Ala"		
XX			
FN	WO2000054573-Al.		
XX			
PD	21-SEP-2000.		
XX			
PF	15-MAR-2000; 2000WO-US06759.		
XX			
PR	18-MAR-1999; 99US-0125004.		
PR	09-APR-1999; 99US-0289346.		
XX	(UYNC-) UNIV NORTH CAROLINA STATE.		
PA			
PI	Hanley-Bowdoin L, Orozco BM, Kong L;		
XX			
DR	WPI; 2000-618851/59.		
XX			
PT	Transgenic plants with increased resistance to geminivirus infection		

PT comprise a nucleic acid construct containing a nucleic acid sequence  
PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
XX  
XX  
XX Disclosure; Page 48; 73pp; English.  
XX  
CC The present sequence represents a mutant peptide, derived from a  
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
CC protein are used to produce transgenic plants. The mutation in AL1 is  
CC present in a ribosome binding region, and expression of mutant AL1  
CC protein imparts increased resistance to geminivirus infection in the  
CC plant. Mutant AL1 proteins are useful for producing plants having  
CC increased resistance or reduced sensitivity to a geminivirus such as  
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
CC virus, cotton leaf curl virus or beet curly top virus.  
XX  
SQ Sequence 70 AA;  
Query Match 92.2%; Score 329; DB 21; Length 70;  
Best Local Similarity 92.9%; Pred. No. 4.6e-34;  
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 TLVWGEFQVDSRGSGCQTNDAAAEALNASSKEEALQIREKIPKYLFAFALNSNL 60  
DB 1 TLVWGEFQVDSRGSGCAASNDAAAEALNASSKEEALQIREKIPKYLQFHNLSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70  
RESULT 6  
AAB18692  
ID AAB18692 standard; peptide; 70 AA.  
XX  
AC AAB18692;  
XX  
XX 22-JAN-2001 (first entry)  
XX  
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
XX  
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
XX ribosome binding region; resistance; geminivirus infection.  
XX  
XX Synthetic.  
XX Tomato golden mosaic virus.  
XX  
XX Key Location/Qualifiers  
FH FT Misc-difference 66 /note= "wild type residue replaced with Ala"  
FT FT Misc-difference 69 /note= "wild type residue replaced with Ala"  
FT FT Misc-difference 69 /note= "wild type residue replaced with Ala"  
XX  
XX WO200054573-A1.  
XX  
XX 21-SEP-2000.  
XX  
XX 15-MAR-2000; 2000WO-US06759.  
XX  
XX 18-MAR-1999; 99US-0125004.  
XX 09-APR-1999; 99US-0289346.  
XX  
XX (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hanley-Bowdoin L, Orozco BM, Kong L;  
XX WPI; 2000-618851/59.  
XX

PT Transgenic plants with increased resistance to geminivirus infection  
PT comprise a nucleic acid construct containing a nucleic acid sequence  
PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
XX  
XX  
XX Disclosure; Page 50; 73pp; English.  
XX  
CC The present sequence represents a mutant peptide, derived from a  
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
CC protein are used to produce transgenic plants. The mutation in AL1 is  
CC present in a ribosome binding region, and expression of mutant AL1  
CC protein imparts increased resistance to geminivirus infection in the  
CC plant. Mutant AL1 proteins are useful for producing plants having  
CC increased resistance or reduced sensitivity to a geminivirus such as  
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
CC virus, cotton leaf curl virus or beet curly top virus.  
XX  
SQ Sequence 70 AA;  
Query Match 91.9%; Score 328; DB 21; Length 70;  
Best Local Similarity 92.9%; Pred. No. 6.1e-34;  
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 TLVWGEFQVDSRGSGCQTNDAAAEALNASSKEEALQIREKIPKYLFAFALNSNL 60  
DB 1 TLVWGEFQVDSRGSGCQTNSNDAAAEALNASSKEEALQIREKIPKYLQFHNLSNL 60  
QY 61 DRIFDKTPEP 70  
DB 61 DRIFDKTPEP 70  
RESULT 7  
AAB18684  
ID AAB18684 standard; peptide; 70 AA.  
XX  
AC AAB18684;  
XX  
XX 22-JAN-2001 (first entry)  
XX  
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
XX  
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
XX ribosome binding region; resistance; geminivirus infection.  
XX  
XX Synthetic.  
XX Tomato golden mosaic virus.  
XX  
XX Key Location/Qualifiers  
FH FT Misc-difference 7 /note= "wild type residue replaced with Ala"  
FT FT Misc-difference 8 /note= "wild type residue replaced with Ala"  
FT FT Misc-difference 8 /note= "wild type residue replaced with Ala"  
XX  
XX WO200054573-A1.  
XX  
XX 21-SEP-2000.  
XX  
XX 15-MAR-2000; 2000WO-US06759.  
XX  
XX 18-MAR-1999; 99US-0125004.  
XX 09-APR-1999; 99US-0289346.  
XX  
XX (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hanley-Bowdoin L, Orozco BM, Kong L;  
XX WPI; 2000-618851/59.  
XX

XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX  
 XX Claim 52; Page 45; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;  
 Query Match 91.3%; Score 326; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 1.1e-33;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEALQIIREKIPEKYLPAALNSNL 60  
 DB 1 TLVWGEAAVDGSARGGCGQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLNSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 8  
 AAB18690  
 ID AAB18690 standard; peptide; 70 AA.  
 AC AAB18690;  
 XX  
 XX 22-JAN-2001 (first entry)  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 27  
 FT /note= "wild type residue replaced with Ala"  
 FT Misc-difference 30  
 FT /note= "wild type residue replaced with Ala"  
 XX  
 XX WO200054573-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 XX 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX

DR WPI; 2000-618951/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX  
 XX Disclosure; Page 49; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;  
 Query Match 91.3%; Score 326; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 1.1e-33;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEALQIIREKIPEKYLPAALNSNL 60  
 DB 1 TLVWGEFQVDSARGGCGQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLNSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 9  
 AAB18678  
 ID AAB18678 standard; peptide; 70 AA.  
 AC AAB18678;  
 XX  
 XX 22-JAN-2001 (first entry)  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 12  
 FT /note= "wild type residue replaced with Ala"  
 FT Misc-difference 13  
 FT /note= "wild type residue replaced with Ala"  
 FT Misc-difference 15  
 FT /note= "wild type residue replaced with Ala"  
 XX  
 XX WO200054573-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 XX 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX

XX  
PI Hanley-Bowdoin L, Orozco BM, Kong L;  
XX WPI; 2000-618851/59.  
DR Transgenic plants with increased resistance to geminivirus infection  
XX comprise a nucleic acid construct containing a nucleic acid sequence  
PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
PT  
XX  
XX Claim 53; Page 42-43; 73pp; English.  
PS  
XX The present sequence represents a mutant peptide, derived from a  
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
CC protein are used to produce transgenic plants. The mutation in AL1 is  
CC present in a ribosome binding region, and expression of mutant AL1  
CC protein imparts increased resistance to geminivirus infection in the  
CC plant. Mutant AL1 proteins are useful for producing plants having  
CC increased resistance or reduced sensitivity to a geminivirus such as  
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
CC virus, cotton leaf curl virus or beet curly top virus.  
XX  
SQ Sequence 70 AA;  
Query Match 91.0%; Score 325; DB 21; Length 70;  
Best Local Similarity 91.4%; Pred. No. 1.5e-33;  
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 TLVWGEFQVDRSGAGCGCQTSDAAALNASSKEEALQIIREKIPKYLFAFAALNSNL 60  
Db 1 TLVWGEFQVDRSGAGCGCQTSDAAALNASSKEEALQIIREKIPKYLFAFAALNSNL 60  
Qy 61 DRIFDKTPEP 70  
Db 61 DRIFDKTPEP 70  
RESULT 10  
AAB18686  
ID AAB18686 standard; peptide; 70 AA.  
XX  
XX AAB18686;  
AC  
XX  
DT 22-JAN-2001 (first entry)  
XX  
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
XX ribosome binding region; resistance; geminivirus infection.  
XX  
XX Synthetic.  
OS Tomato golden mosaic virus.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 24 /note= "wild type residue replaced with Leu"  
FT Misc-difference 25 /note= "wild type residue replaced with Leu"  
FT Misc-difference 26 /note= "wild type residue replaced with Leu"  
FT  
XX  
XX WO200054573-A1.  
XX  
XX 21-SEP-2000.  
XX  
XX 15-MAR-2000; 2000WO-US06759.  
XX  
XX 18-MAR-1999; 99US-0125004.  
XX

PR  
XX  
XX  
PA (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hanley-Bowdoin L, Orozco BM, Kong L;  
XX WPI; 2000-618851/59.  
DR Transgenic plants with increased resistance to geminivirus infection  
XX comprise a nucleic acid construct containing a nucleic acid sequence  
PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
PT  
XX  
XX Claim 53; Page 46; 73pp; English.  
PS  
XX The present sequence represents a mutant peptide, derived from a  
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
CC protein are used to produce transgenic plants. The mutation in AL1 is  
CC present in a ribosome binding region, and expression of mutant AL1  
CC protein imparts increased resistance to geminivirus infection in the  
CC plant. Mutant AL1 proteins are useful for producing plants having  
CC increased resistance or reduced sensitivity to a geminivirus such as  
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
CC virus, cotton leaf curl virus or beet curly top virus.  
XX  
SQ Sequence 70 AA;  
Query Match 91.0%; Score 325; DB 21; Length 70;  
Best Local Similarity 91.4%; Pred. No. 1.5e-33;  
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
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Db 1 TLVWGEFQVDRSGAGCGCQTSDAAALNASSKEEALQIIREKIPKYLFAFAALNSNL 60  
Qy 61 DRIFDKTPEP 70  
Db 61 DRIFDKTPEP 70  
RESULT 11  
AAB18689  
ID AAB18689 standard; peptide; 70 AA.  
XX  
XX AAB18689;  
AC  
XX  
XX 22-JAN-2001 (first entry)  
DT  
XX  
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
XX ribosome binding region; resistance; geminivirus infection.  
XX  
XX Synthetic.  
OS Tomato golden mosaic virus.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 22 /note= "wild type residue replaced with Ala"  
FT Misc-difference 23 /note= "wild type residue replaced with Ala"  
FT  
XX  
XX WO200054573-A1.  
XX  
XX 21-SEP-2000.  
XX  
XX 15-MAR-2000; 2000WO-US06759.  
XX



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PN WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Disclosure; Page 49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
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XX Best Local Similarity 91.4%; Pred. No. 3.5e-33;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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XX Db 1 TLVWGEFQVDRSGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60
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XX Qy 61 DRIFDKTPEP 70
XX Db 61 DRIFDKTPEP 70
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XX RESULT 14
XX AAB18681
XX ID AAB18681 standard; peptide; 70 AA.
XX AC AAB18681;
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XX XX 22-JAN-2001 (first entry)
XX
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX
XX XX Key Location/Qualifiers
XX FT Misc-difference 47 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 48 /note= "wild type residue replaced with Ala"
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FT Misc-difference 49 /note= "wild type residue replaced with Ala"
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XX PN WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 52; Page 44; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 89.4%; Score 319; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 8.5e-33;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX Qy 1 TLVWGEFQVDRSGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60
XX Db 1 TLVWGEFQVDRSGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60
XX
XX Qy 61 DRIFDKTPEP 70
XX Db 61 DRIFDKTPEP 70
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XX RESULT 15
XX AAB18683
XX ID AAB18683 standard; peptide; 70 AA.
XX AC AAB18683;
XX
XX XX 22-JAN-2001 (first entry)
XX
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX
XX XX Key Location/Qualifiers
XX FT Misc-difference 59
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FT Misc-difference 61 /note= "wild type residue replaced with Ala"  
FT /note= "wild type residue replaced with Ala"  
FT Misc-difference 62  
FT /note= "wild type residue replaced with Ala"  
XX

FN WO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

PR 09-APR-1999; 99US-0289346.

XX (UYNCL) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

Transgenic plants with increased resistance to geminivirus infection  
comprise a nucleic acid construct containing a nucleic acid sequence  
encoding a mutant AL1 protein with a mutation in the Rb binding region

Claim 53; Page 45; 73pp; English.

The present sequence represents a mutant peptide, derived from a  
geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
DNA, and interacts with other viral and host proteins. Mutants of the AL1  
protein are used to produce transgenic plants. The mutation in AL1 is  
present in a ribosome binding region, and expression of mutant AL1  
protein imparts increased resistance to geminivirus infection in the  
plant. Mutant AL1 proteins are useful for producing plants having  
increased resistance or reduced sensitivity to a geminivirus such as  
tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
virus, cotton leaf curl virus or beet curly top virus.

SQ Sequence 70 AA;

Query Match 89.1%; Score 318; DB 21; Length 70;  
Best Local Similarity 91.4%; Pred. No. 1.1e-32;  
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDCRSARGGCGTNDAAAEALNASSKEEALQIREKIPEKYLFAFALNSNL 60  
Db 1 TLVWGEFQVDCRSARGGCGTNDAAAEALNASSKEEALQIREKIPEKYLFOFHNSAL 60

Qy 61 DRIFDKTPEP 70

Db 61 AAIFDKTPEP 70

Search completed: December 23, 2003, 08:56:30  
Job time : 32.6667 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 11.6667 Seconds  
(without alignments)  
253.865 Million cell updates/sec

Title: US-09-289-346B-6  
Perfect score: 357  
Sequence: 1 TLVWGEFQVGRSARGCQT.....FAFALNSNLDRIPTKTEP 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*  
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4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*  
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6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	210	58.8	359	3	US-08-809-103B-2 Sequence 2, Appli
2	210	58.8	359	3	US-08-809-103B-4 Sequence 4, Appli
3	210	58.8	359	3	US-08-809-103B-6 Sequence 6, Appli
4	210	58.8	359	3	US-08-809-103B-8 Sequence 8, Appli
5	206	57.7	353	3	US-08-838-151A-44 Sequence 44, Appli
6	206	57.7	353	3	US-08-838-151A-46 Sequence 46, Appli
7	206	57.7	353	3	US-08-838-151A-49 Sequence 49, Appli
8	206	57.7	353	3	US-08-838-151A-52 Sequence 52, Appli
9	206	57.7	353	3	US-08-838-151A-55 Sequence 55, Appli
10	204	57.1	361	3	US-08-838-151A-2 Sequence 2, Appli
11	204	57.1	361	3	US-08-838-151A-4 Sequence 4, Appli
12	204	57.1	361	3	US-08-838-151A-6 Sequence 6, Appli
13	204	57.1	361	3	US-08-838-151A-8 Sequence 8, Appli
14	191	53.5	357	3	US-08-838-151A-24 Sequence 24, Appli
15	191	53.5	357	3	US-08-838-151A-27 Sequence 27, Appli
16	191	53.5	357	3	US-08-838-151A-30 Sequence 30, Appli
17	183	51.3	357	3	US-08-838-151A-20 Sequence 20, Appli
18	67	18.8	447	4	US-09-996-243-369 Sequence 369, App
19	67	18.8	447	4	US-09-482-273-128 Sequence 128, App
20	67	18.8	456	4	US-09-482-273-229 Sequence 229, App
21	64.5	18.1	1713	3	US-08-600-982-24 Sequence 24, Appli
22	64.5	18.1	1713	3	PCT-US94-10261A-24 Sequence 24, Appli
23	63.5	17.8	2161	1	US-07-745-206A-2 Sequence 2, Appli
24	63.5	17.8	2161	1	US-08-455-543A-49 Sequence 49, Appli
25	63.5	17.8	2161	1	US-08-455-543A-51 Sequence 51, Appli
26	63.5	17.8	2161	2	US-08-223-305C-49 Sequence 49, Appli
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28	63.5	17.8	2161	2	US-08-311-363-2 Sequence 2, Appli
29	63	17.6	293	4	US-09-414-276-3 Sequence 3, Appli
30	63	17.6	335	4	US-09-414-276-6 Sequence 6, Appli
31	60.5	16.9	131	3	US-08-838-151A-14 Sequence 14, Appli
32	60.5	16.9	244	4	US-09-328-352-4541 Sequence 4541, Ap
33	60	16.8	531	4	US-08-976-063B-34 Sequence 34, Appli
34	58.5	16.4	1203	4	US-09-351-200-2 Sequence 2, Appli
35	58	16.2	173	4	US-09-266-225D-2 Sequence 2, Appli
36	58	16.2	446	3	US-08-672-814D-11 Sequence 11, Appli
37	58	16.2	446	3	US-09-333-696-11 Sequence 11, Appli
38	58	16.2	446	4	US-09-282-218A-19 Sequence 19, Appli
39	55.5	15.5	426	4	US-09-252-991A-20262 Sequence 20262, A
40	55.5	15.5	593	3	US-09-234-393-54 Sequence 54, Appli
41	55.5	15.5	593	4	US-09-865-171-54 Sequence 54, Appli
42	55	15.4	288	4	US-09-328-352-6485 Sequence 6485, Ap
43	55	15.4	374	3	US-09-091-405-2 Sequence 2, Appli
44	55	15.4	498	2	US-08-511-485-13 Sequence 13, Appli
45	55	15.4	498	4	US-09-201-936-13 Sequence 13, Appli

ALIGNMENTS

RESULT 1  
US-08-809-103B-2  
; Sequence 2, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GROENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,103B  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR95/01192  
; FILING DATE: 15-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: US894AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-809-103B-2

Query Match 58.8%; Score 210; DB 3; Length 359;  
Best Local Similarity 56.5%; Pred. No. 4.8e-20;  
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

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QY 2 LVWGEFQVDSRGSGCOTSDAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNLD 61
Db 111 LEWGTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170
QY 62 RIFDKTPEP 70
Db 171 KVQVPPAP 179

RESULT 2
US-08-809-103B-4
; Sequence 4, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: FR 94.11040
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-4

Query Match 58.8%; Score 210; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 4.8e-20;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDSRGSGCOTSDAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNLD 61
Db 111 LEWGTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170
QY 62 RIFDKTPEP 70
Db 171 KVQVPPAP 179

RESULT 3
US-08-809-103B-6
; Sequence 6, Application US/08809103B
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; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: FR 94.11040
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-6

Query Match 58.8%; Score 210; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 4.8e-20;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDSRGSGCOTSDAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNLD 61
Db 111 LEWGTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNHNSNLD 170
QY 62 RIFDKTPEP 70
Db 171 KVQVPPAP 179

RESULT 4
US-08-809-103B-8
; Sequence 8, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/809,103B
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8

Query Match 58.8%; Score 210; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 4.8e-20;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVWGFEQVDSARGGCGTSDNAAEALNASSKEEALQIIREKIPEKYLPAFAALNSLD 61
Db 111 LEWGTFFQDGRSARGGQTANDAYAKAINAGSKSQALDVKEIAPRDYVLFHFNINSMD 170

Qy 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

RESULT 5
US-08-838-151A-44
; Sequence 44, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

Query Match 57.7%; Score 206; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.6e-19;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-44

Query Match 57.7%; Score 206; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.6e-19;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TLWGEFQVDSARGGCGTSDNAAEALNASSKEEALQIIREKIPEKYLPAFAALNSNL 60
Db 110 TIWGEFQVDSARGGCGTSDNAAEALNASSKEEALQIIREKIPEKYLPAFAALNSNL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 6
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

Query Match 57.7%; Score 206; DB 3; Length 353;
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-55

Query Match          57.7%; Score 206; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.6e-19;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

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Db 110 TIEMGFQV DGRSARGG CQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 169

QY 61 DRIFDKTPEP 70
   :|||:|||:|||
Db 170 ERIFVKVPEP 179

RESULT 10
US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-55

Query Match          57.7%; Score 206; DB 3; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.6e-19;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGEFQV DGRSARGG CQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 60
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Db 110 TIEMGFQV DGRSARGG CQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 169

QY 61 DRIFDKTPEP 70
   :|||:|||:|||
Db 170 ERIFVKVPEP 179

RESULT 11
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match          57.1%; Score 204; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.1e-19;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQV DGRSARGG CQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 60
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 110 TIEMGFQV DGRSARGG CQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 169
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-2

Query Match          57.1%; Score 204; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.1e-19;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQV DGRSARGG CQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 60
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Db 110 TIEMGFQV DGRSARGG CQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 169

QY 61 DRIFDKTPEP 70
   :|||:|||:|||
Db 170 ERIFAKAPEP 179

RESULT 11
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match          57.1%; Score 204; DB 3; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.1e-19;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQV DGRSARGG CQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 60
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 110 TIEMGFQV DGRSARGG CQTSDNDAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 169
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QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 12
US-08-838-151A-6
; Sequence 6, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8
; Query Match 57.1%; Score 204; DB 3; Length 361;
; Best Local Similarity 54.3%; Pred. No. 3.1e-19;
; Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0

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QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 14
US-08-838-151A-24
; Sequence 24, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6
; Query Match 57.1%; Score 204; DB 3; Length 361;
; Best Local Similarity 54.3%; Pred. No. 3.1e-19;
; Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0

QY 1 TLVWGEFQDGRSARGCGQTSNDAAALNASSKEALQIIREKIPKYLFAFALNSNL 60
Db 110 TIWGDFFQIDGRSARGGQGSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNRSL 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 13
US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus

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; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-24

Query Match          53.5%; Score 191; DB 3; Length 357;
Best Local Similarity 62.3%; Pred. No. 1.7e-17;
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

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Db      111 FGVSQIDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPKYLFAFAALNSNLDRI 170

Qy      64 F 64
Db      171 F 171

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; RESULT 15
; US-08-838-151A-27
; Sequence 27, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-27
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Query Match          53.5%; Score 191; DB 3; Length 357;
Best Local Similarity 62.3%; Pred. No. 1.7e-17;
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

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Db      111 FGVSQIDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPKYLFAFAALNSNLDRI 170

Qy      64 F 64
Db      171 F 171
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Search completed: December 23, 2003, 08:59:34  
Job time : 11.6667 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds

(without alignments)  
172.015 Million cell updates/sec

Title: US-09-289-346B-6

Perfect score: 357

Sequence: 1 TLVWGFQVDSARGGCGT.....FAFAALNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	332	93.0	70	10	US-09-289-346A-9
5	329	92.2	70	10	US-09-289-346A-12
6	328	91.9	70	10	US-09-289-346A-16
7	326	91.3	70	10	US-09-289-346A-8
8	326	91.3	70	10	US-09-289-346A-14
9	325	91.0	70	10	US-09-289-346A-2
10	325	91.0	70	10	US-09-289-346A-10
11	324	90.8	70	10	US-09-289-346A-13
12	322	90.2	70	10	US-09-289-346A-4
13	322	90.2	70	10	US-09-289-346A-15
14	319	89.4	70	10	US-09-289-346A-5
15	318	89.1	70	10	US-09-289-346A-7

16	308	86.3	70	10	US-09-289-346A-3
17	67	18.8	447	9	US-09-989-722-369
18	67	18.8	447	9	US-09-989-723-369
19	67	18.8	447	9	US-09-989-279-369
20	67	18.8	447	9	US-09-989-727-369
21	67	18.8	447	10	US-09-989-731-369
22	67	18.8	447	10	US-09-989-732-369
23	67	18.8	447	10	US-09-991-073-369
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25	67	18.8	447	10	US-09-991-163-369
26	67	18.8	447	10	US-09-993-604-369
27	67	18.8	447	10	US-09-990-456-369
28	67	18.8	447	10	US-09-989-721-369
29	67	18.8	447	10	US-09-992-598-369
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31	67	18.8	447	10	US-09-989-735-369
32	67	18.8	447	10	US-09-990-444-369
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36	67	18.8	447	10	US-09-993-687-369
37	67	18.8	447	11	US-09-989-734-369
38	67	18.8	447	11	US-09-997-653-369
39	67	18.8	447	11	US-09-993-667-369
40	67	18.8	447	11	US-09-997-428-369
41	67	18.8	447	11	US-09-997-666-369
42	67	18.8	447	11	US-09-990-438-369
43	67	18.8	447	11	US-09-990-562-369
44	67	18.8	447	11	US-09-990-711-369
45	67	18.8	447	11	US-09-984-271-128

ALIGNMENTS

RESULT 1

US-09-289-346A-6  
; Sequence 6, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-die  
; APPLICANT: Gruijssem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (52)..(55)  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
; OTHER INFORMATION: TGMV Protein (aa 110-179) with alanine  
; OTHER INFORMATION: replacements (QFHN165->AFAA165).  
US-09-289-346A-6

Query Match	100.0%;	Score 357;	DB 10;	Length 70;
Best Local Similarity	100.0%;	Pred. No. 3.9e-39;		
Matches	70;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	TLVWGFQVDSARGGCGTSDNDAABALNASSKEEALQIREKIPKYLFAFAALNSNL	60	
Db	1	TLVWGFQVDSARGGCGTSDNDAABALNASSKEEALQIREKIPKYLFAFAALNSNL	60	
Qy	61	DRIFDKTPEP	70	

```
Db          110 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFPHNLNSNL 169
QY          61 DRIFDKTPEP 70
          |||||
Db          170 DRIFDKTPEP 179

RESULT 4
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9

Query Match          93.0%; Score 332; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 7.3e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY          1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFPHNLNSNL 60
Db          1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFPHNLNSNL 60
QY          61 DRIFDKTPEP 70
          |||||
Db          61 DRIFDKTPEP 70

RESULT 5
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12

Query Match          92.2%; Score 329; DB 10; Length 70;

Db          110 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFPHNLNSNL 169
QY          61 DRIFDKTPEP 70
          |||||
Db          170 DRIFDKTPEP 179

RESULT 4
US-09-289-346A-1
; Sequence 1, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-1

Query Match          95.2%; Score 340; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 6.5e-37;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFPHNLNSNL 60
Db          1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFPHNLNSNL 60
QY          61 DRIFDKTPEP 70
          |||||
Db          61 DRIFDKTPEP 70

RESULT 3
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11

Query Match          95.2%; Score 340; DB 10; Length 356;
Best Local Similarity 95.7%; Pred. No. 5.7e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFPHNLNSNL 60
          |||||
```

```
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->AA118).
US-09-289-346A-8

Query Match          91.3%; Score 326; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 4.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||
Db 1 TLVWGFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 6
US-09-289-346A-16
; Sequence 16, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-16

Query Match          91.9%; Score 328; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 2.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||
Db 1 TLVWGFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 7
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)..(8)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
```

```
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->AA118).
US-09-289-346A-8

Query Match          91.3%; Score 326; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 4.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||
Db 1 TLVWGFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 8
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14

Query Match          91.3%; Score 326; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 4.4e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||
Db 1 TLVWGFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPKYLFAFAALNSNL 60
   |||||

QY 61 DRIFDKTPEP 70
   |||||
Db 61 DRIFDKTPEP 70
   |||||

RESULT 9
US-09-289-346A-2
; Sequence 2, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
```

```
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
US-09-289-346A-2

Query Match          91.0%; Score 325; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 6e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCOTSDNDAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
DB 1 TLVWGEFQVDRSARGGCOTSDNDAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAAL36->LLLL136).
US-09-289-346A-10

Query Match          91.0%; Score 325; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 6e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCOTSDNDAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
DB 1 TLVWGEFQVDRSARGGCOTSDNLLLEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm

; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (42)..(44)
; OTHER INFORMATION: Description of Artificial sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REK154->AAA154).
US-09-289-346A-4

Query Match          90.2%; Score 322; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.5e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCOTSDNDAAEALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
DB 1 TLVWGEFQVDRSARGGCOTSDNDAAEALNASSKEEALQIIRAAAIPKYLFAFALNSNL 60

QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match      90.2%; Score 322; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.5e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60
Db      1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60

Qy      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

RESULT 14
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (EKY159->AAA159).
US-09-289-346A-5

Query Match      89.4%; Score 319; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 3.7e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60
Db      1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPAAALFQFHNLSNL 60

Qy      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

```

```

RESULT 15
US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (59)..(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDRI72->ALAAI72).
US-09-289-346A-7

Query Match      89.1%; Score 318; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 4.9e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNL 60
Db      1 TLVWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLSAL 60

Qy      61 DRIFDKTPEP 70
Db      61 AAIFDKTPEP 70

Search completed: December 23, 2003, 09:43:30
Job time : 77 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds  
(without alignments)  
673.181 Million cell updates/sec

Title: US-09-289-346B-6  
Perfect score: 357  
Sequence: 1 TLVWGEFQVDSARGGCQT.....FAFAALNSLDRIFDKTPEP 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	340	95.2	352	1 QQCVL1	Al1 protein - toma
2	240	67.2	361	1 QQCVP	Al1 protein - pota
3	227	63.6	358	2 S07594	hypothetical prote
4	220	61.6	362	1 JQ1887	Al1 protein - toma
5	217	60.8	359	2 S39211	gene Cl protein -
6	212	59.4	351	2 JQ2327	Al1 protein - Indi
7	210	58.8	359	2 S22593	hypothetical prote
8	209	58.5	349	2 JQ2300	replicase - pepper
9	209	58.5	349	2 S31875	Al1 protein - pepp
10	204	57.1	359	2 S39235	gene Cl protein -
11	203	56.9	355	1 QQCVM1	AV1 protein - abut
12	200	56.0	358	1 JQ1870	Al1 protein - toma
13	200	56.0	385	2 S28360	Al1 protein - beet
14	193	54.1	360	2 S59885	replication-associ
15	191	53.5	357	1 QQCVC1	Al1 protein - toma
16	118	33.1	131	2 S45059	AC1 protein (clone
17	104	29.1	347	1 QQCVS1	Al1 protein - squa
18	67	18.8	447	2 T12544	hypothetical prote
19	64.5	18.1	587	2 JC419	Pc gamma (19G) rec
20	64.5	18.1	1713	2 A55347	adhesive ligand ep
21	63.5	17.8	180	2 D84082	hypothetical prote
22	63.5	17.8	1610	2 A46227	voltage-dependent
23	63.5	17.8	1646	2 JH0422	voltage-dependent
24	63.5	17.8	2161	2 JH0564	calcium channel al
25	63.5	17.8	2181	2 A38198	calcium channel al
26	63.5	17.8	2203	2 T42742	voltage-dependent
27	63	17.6	316	2 C82085	conserved hypothet
28	62.5	17.5	1033	2 E97700	hypothetical prote
29	62	17.4	338	2 AG3582	iron(III)-binding

probably O-sialogl  
acetyl-CoA C-acety  
probable large ATP  
protein-Npi-phosph  
YNT20 protein - ye  
Cl protein - tobac  
phytoene synthase  
phytoene synthase  
probable ferrichro  
phage-related prot  
zinc finger protei  
probable peptidyl-  
gamma-aminobutyrat  
diaminobutyrate-py  
hypothetical prote  
hypothetical prote

30 62 17.4 340 2 B97011  
31 61.5 17.2 392 2 T45290  
32 60.5 16.9 840 2 T36175  
33 60 16.8 154 2 AD3475  
34 60 16.8 269 2 S61633  
35 60 16.8 295 2 D42452  
36 60 16.8 355 2 S49621  
37 60 16.8 355 2 T50746  
38 60 16.8 714 2 C95382  
39 60 16.8 827 2 D96907  
40 60 16.8 1888 2 T14273  
41 59.5 16.7 299 2 B71967  
42 59.5 16.7 470 2 T46814  
43 59.5 16.7 470 2 B95419  
44 59.5 16.7 2137 2 T05244  
45 59.5 16.7 4385 2 T29042

ALIGNMENTS

RESULT 1

QCCVL1  
Al1 protein - tomato golden mosaic virus  
C:Species: tomato golden mosaic virus  
A:Note: host Nicotiana sp. (tobacco)  
C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Apr-1994  
C:Accession: A04170  
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.  
EMBO J. 3, 2197-2205, 1984  
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat  
A:Reference number: A04163  
A:Accession: A04170  
A:Molecule type: DNA  
A:Residues: 1-352 <HAM>  
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 95.2%; Score 340; DB 1; Length 352;  
Best Local Similarity 95.7%; Pred. No. 4.5e-31;  
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCQTSNDAAALNASSKEALQIIREKIPEKYLFAFALNSNL 60  
|||||  
Db 111 TLVWGEFQVDSARGGCQTSNDAAALNASSKEALQIIREKIPEKYLFOFHLNSNL 170  
|||||

QY 61 DRIFDKTPEP 70  
|||||  
Db 171 DRIFDKTPEP 180  
|||||

RESULT 2

QCCVPT  
Al1 protein - potato yellow mosaic virus (isolate Venezuela)  
C:Species: potato yellow mosaic virus  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jun-2000  
C:Accession: JU0364  
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.  
J. Gen. Virol. 72, 1515-1520, 1991  
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel  
A:Reference number: JU0362; MUID:91311403; PMID:1856690  
A:Accession: JU0364  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-361 <COU>  
A:Cross-references: GB:D00940; NID:g222458; PIDN:BAA00782.1; PID:g222459  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 67.2%; Score 240; DB 1; Length 361;  
Best Local Similarity 66.7%; Pred. No. 1.2e-19;  
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGCOTSDAAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60  
DB 110 TIEWGLFQIDGRSARGCGQTVNDAAEALNSGTKEAMKIIKEKLPKFLFOYHNLSCNL 169

QY 61 DRIFDKTPEP 69  
DB 170 DRIFDKAPE 178

RESULT 3  
S07594  
hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)  
C:Species: cassava latent virus  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Sep-1999  
C:Accession: S07594  
R:Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.  
Nucleic Acids Res. 18, 197-198, 1990  
A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava  
A:Reference number: S07590; MUID:90174930; PMID:2308831  
A:Accession: S07594  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-358 <NOR>  
A:Cross-references: EMBL:X17095; NID:g59371; PIDN:CAA34953.1; PID:g59376  
C:Genetics:  
A:Map position: segment DNAL  
C:Superfamily: tomato golden mosaic virus All protein

Query Match 63.6%; Score 227; DB 2; Length 358;  
Best Local Similarity 60.8%; Pred. No. 3.6e-18;  
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGCGCOTSDAAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60  
DB 109 TVEWGQFQIDGRSARGCGQSANDAYAKALNSGSKSEALNVLRLAPKDYVLQFHNLSNL 168

QY 61 DRIFDKTPEP 70  
DB 169 DRIFQPEPPAP 178

RESULT 4  
JQ1887  
All protein - tomato yellow leaf curl virus (strain Australia)  
N:Alternate names: CI protein  
C:Species: tomato yellow leaf curl virus  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 07-May-1999  
C:Accession: JQ1887  
R:Dy, I.B.; Rigden, J.E.; Krake, L.R.; Mullineaux, P.M.; Rezaian, M.A.  
J. Gen. Virol. 74, 147-151, 1993  
A:Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.  
A:Reference number: JQ1885; MUID:93139778; PMID:8423446  
A:Accession: JQ1887  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-362 <DRY>  
A:Cross-references: GB:S53251  
C:Superfamily: tomato golden mosaic virus All protein

Query Match 61.6%; Score 220; DB 1; Length 362;  
Best Local Similarity 52.9%; Pred. No. 2.3e-17;  
Matches 45; Conservative 9; Mismatches 15; Indels 16; Gaps 1;

QY 1 TLVWGEFQVDSARGCGCOTSDAAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 60  
DB 110 TIEWGEFQIDGRSARGCGQSANDAYAKALNSGSKSEALNVLRLAPKDYVLQFHNLSNL 169

QY 61 DRI-----FDKTPPE 69  
|||

DB 170 DRIFTPPLEVTVSPFLSSSDFRVPE 194

RESULT 5  
S39211  
Gene CI protein - tomato yellow leaf curl virus  
C:Species: tomato yellow leaf curl virus  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Sep-1999  
C:Accession: S39211  
R:Norris, B.; Hidalgo, B.; Accotto, G.; Moriones, E.  
submitted to the EMBL Data Library, August 1993  
A:Description: High similarity among the tomato yellow leaf curl virus isolates from th  
A:Reference number: S39209  
A:Accession: S39211  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-359 <NOR>  
A:Cross-references: EMBL:Z25751; NID:g433655; PIDN:CAA81026.1; PID:g433658  
C:Superfamily: tomato golden mosaic virus All protein

Query Match 60.8%; Score 217; DB 2; Length 359;  
Best Local Similarity 59.4%; Pred. No. 5.1e-17;  
Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDSARGCGCOTSDAAAEALNASSKEEALQIIREKIPKYLFAFALNSNL 61  
DB 111 LEWGTQFQIDGRSARGCGQTANDAYAKALNAGSKSEALDVIKELAPRDYILHFHNSNL 170

QY 62 RIFDKTPEP 70  
DB 171 RVFQVPPAP 179

RESULT 6  
JQ2327  
All protein - Indian cassava mosaic virus  
N:Alternate names: replication-associated protein  
C:Species: Indian cassava mosaic virus  
C:Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 20-Sep-1999  
C:Accession: JQ2327; S35883  
R:Hong, Y.G.; Robinson, D.J.; Harrison, B.D.  
J. Gen. Virol. 74, 2437-2443, 1993  
A:Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-tra  
A:Reference number: JQ2326; MUID:94085670; PMID:8245859  
A:Accession: JQ2327  
A:Molecule type: DNA  
A:Residues: 1-351 <HON>  
A:Cross-references: EMBL:Z24758; NID:g395351; PIDN:CAA80891.1; PID:g584046  
C:Superfamily: tomato golden mosaic virus All protein

Query Match 59.4%; Score 212; DB 2; Length 351;  
Best Local Similarity 62.7%; Pred. No. 1.8e-16;  
Matches 42; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 4 WGEFQVDSARGCGCOTSDAAAEALNASSKEEALQIIREKIPKYLFAFALNSLDRI 63  
DB 113 WGTQFQIDGRSARGCGQSANDAYAKALNSGSKSEALKIRLAPRDYILRDFHHSNLDRI 172

QY 64 FDKTPEP 70  
DB 173 FTKPPPP 179

RESULT 7  
S22593  
hypothetical protein C4 - tomato yellow leaf curl virus  
C:Species: tomato yellow leaf curl virus  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Sep-1999  
C:Accession: S22593  
R:Kheyr-pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, E  
Nucleic Acids Res. 19, 6763-6769, 1991  
A:Title: Tomato yellow leaf curl virus from Sardinia is a whitefly transmitted monopart  
A:Reference number: S22588; MUID:92107660; PMID:1840676

A;Accession: S22593  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-359 <KHE>  
A;Cross-references: EMBL:X61153; NID:G62211; PIDN:CAA43466.1; PID:G62217  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991  
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 58.8%; Score 210; DB 2; Length 359;  
Best Local Similarity 56.5%; Pred. No. 3.2e-16;  
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVMGEFQVDSARGGCGTSDNDAAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 61  
Db 111 LVMGEFQVDSARGGCGTSDNDAAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 61

Qy 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

RESULT 8  
JQ2300  
replicase - pepper huasteco virus (component A)  
N;Alternate names: ORF AL1 protein  
C;Species: pepper huasteco virus  
C;Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 20-Sep-1999  
C;Accession: JQ2300  
R;Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Herrera-Estrella, L.; Rivera-Bustamante, R.F.  
J. Gen. Virol. 74, 2225-2231, 1993  
A;Title: Complete nucleotide of pepper huasteco virus: Analysis and comparison with bipa  
A;Reference number: JQ2299; MUID:94015007; PMID:8403944  
A;Accession: JQ2300  
A;Molecule type: DNA  
A;Residues: 1-349 <TOR>  
A;Cross-references: GB:X70418; NID:G61023; PIDN:CAA49856.1; PID:G61025  
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 58.5%; Score 209; DB 2; Length 349;  
Best Local Similarity 57.1%; Pred. No. 4e-16;  
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDSARGGCGTSDNDAAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 60  
Db 110 TVWGEFQIDGRSARGGQGSANDTYAKALNSASAEALQIIRKQPHFFLOFHNIVSNA 169

Qy 61 DRIFDKTPEP 70  
Db 170 NRIFQTPPEP 179

RESULT 9  
S31875  
AL1 protein - pepper rizado amarillo virus  
C;Species: pepper rizado amarillo virus  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 20-Sep-1999  
C;Accession: S31875  
R;Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera-Bu  
submitted to the EMBL Data Library, February 1993  
A;Description: Complete nucleotide sequence of pepper huasteco virus: analysis and compa  
A;Reference number: S31872  
A;Accession: S31875  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-349 <TOR>  
A;Cross-references: EMBL:X70418; NID:G61023; PIDN:CAA49856.1; PID:G61025  
A;Note: the source is designated as pepper huasteco virus  
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 58.5%; Score 209; DB 2; Length 349;  
Best Local Similarity 57.1%; Pred. No. 4e-16;  
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDSARGGCGTSDNDAAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 60  
Db 110 TVWGEFQIDGRSARGGQGSANDTYAKALNSASAEALQIIRKQPHFFLOFHNIVSNA 169

Qy 61 DRIFDKTPEP 70  
Db 170 NRIFQTPPEP 179

RESULT 10  
S39235  
gene C1 protein - tomato yellow leaf curl virus  
C;Species: tomato yellow leaf curl virus  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Sep-1997  
C;Accession: S39235  
R;Crespi, S.; Norris, B.; Vaira, A.; Bosco, D.; Accotto, G.  
submitted to the EMBL Data Library, December 1993  
A;Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.  
A;Reference number: S39233  
A;Accession: S39235  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-359 <CRE>  
A;Cross-references: EMBL:Z28390; NID:G1041671; PID:G1334964  
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 57.1%; Score 204; DB 2; Length 359;  
Best Local Similarity 55.1%; Pred. No. 1.5e-15;  
Matches 38; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Qy 2 LVMGEFQVDSARGGCGTSDNDAAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 61  
Db 111 LEWGTFTQIDGRSARGGCGTANDAYAKAINAKSKSEALDVIKQLAPRDYVHLHFNISNL 170

Qy 62 RIFDKTPEP 70  
Db 171 KVFQVPPAP 179

RESULT 11  
QOCVM1  
A; protein - abutilon mosaic virus (isolate West India)  
C;Species: abutilon mosaic virus  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 08-Apr-1994  
C;Accession: A36214  
R;Frischmuth, T.; Zimmatt, G.; Jeske, H.  
Virology 178, 461-468, 1990  
A;Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as w  
A;Reference number: A36214; MUID:91020984; PMID:2219703  
A;Accession: A36214  
A;Molecule type: DNA  
A;Residues: 1-355 <FRI>  
A;Cross-references: EMBL:X15983  
C;Genetics:  
A;Map position: segment A  
C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 56.9%; Score 203; DB 1; Length 355;  
Best Local Similarity 55.7%; Pred. No. 2e-15;  
Matches 39; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDSARGGCGTSDNDAAAEALNASSKEALQIIREKIPEKYLFAFALNSNL 60  
Db 110 TAEWGEFQIDGRSARGGCGTANDSYAKALNAGDVQSALNLIKBEQPKDVLQNHVIRNSNL 169

Qy 61 DRIFDKTPEP 70  
Db 170 ERIFAKAPEP 179

RESULT 12  
JQ1870  
AL1 protein - tomato mottle virus (isolate Florida)



A;Molecule type: DNA

Db 197 QKIFQRPPDP 206

A;Molecule type: DNA

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds  
(without alignments)  
569.747 Million cell updates/sec

Title: US-09-289-346B-6

Perfect score: 357

Sequence: 1 TLVWGFQVDSARGGCGT.....FAFAALNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	340	95.2	352	1 VAL1_TGMV	P03567 tomato gold
2	240	67.2	361	1 VAL1_PYMV	P27258 potato yell
3	227	63.6	358	1 VAL1_CLVK	P14982 cassava lat
4	227	63.6	358	1 VAL1_CLVN	P14972 cassava lat
5	220	61.6	362	1 VAL1_TYLCU	P36279 tomato yell
6	217	60.8	359	1 VAL1_TYLCU	P38609 tomato yell
7	210	58.8	359	1 VAL1_TYLCM	P27260 tomato yell
8	209	58.5	349	1 VAL1_PHVU	Q06923 pepper huas
9	204	57.1	353	1 VAL1_BGMV	P05175 bean golden
10	203	56.9	355	1 VAL1_BMVW	P21947 abutilon mo
11	200	56.0	358	1 VAL1_BCTV	P14991 beet curly
12	200	56.0	361	1 VAL1_TMOV	Q06657 tomato mott
13	191	53.5	357	1 VAL1_TYLCV	P27259 tomato yell
14	104	29.1	347	1 VAL1_SLVC	Q29048 squash leaf
15	67	18.8	447	1 TBL2_HUMAN	Q9V4P3 homo sapien
16	64.5	18.1	1713	1 LMA3_HUMAN	Q16787 homo sapien
17	63.5	17.8	1610	1 CCAD_MESAU	Q99244 mesocricetu
18	63.5	17.8	2161	1 CCAD_HUMAN	Q01668 homo sapien
19	63.5	17.8	2203	1 CCAD_RAT	P27732 rattus norv
20	62	17.4	476	1 DGR2_HUMAN	Q96df8 homo sapien
21	62	17.4	479	1 DGR2_MOUSE	Q70279 mus musculu
22	60	16.8	269	1 ORN_YEAS	P54964 saccharomyc
23	60	16.8	295	1 VAL1_TYDVA	P31617 tobacco yell
24	60	16.8	355	1 CRTE_RHOSH	P4905 rhodobacter
25	59.5	16.7	299	1 Y175_HELPJ	Q92mq7 helicobacte
26	59.5	16.7	470	1 RHA RHIME	Q923r2 r diaminobu
27	58.5	16.4	127	1 RS11_LACLA	Q9cdv2 lactococcus
28	58.5	16.4	706	1 Y006_RICPR	Q9zed6 rickettsia
29	58.5	16.4	1232	1 YQ05_CABEL	P34643 caenorhabdi
30	58	16.2	207	1 IL6_MARMO	O35736 marmota mon
31	58	16.2	319	1 LDH2_STAAM	Q99r35 staphylococ
32	58	16.2	319	1 LDH2_STAAM	Q8num9 staphylococ
33	58	16.2	447	1 CDSA_DROME	P56079 d phosphati

#### ALIGNMENTS

##### RESULT 1

```

VAL1_TGMV
ID VAL1_TGMV STANDARD; PRT; 352 AA.
AC P03567;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Tomato golden mosaic virus (TGMV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10831;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamilton W.D.O., Stain V.E., Courts R.H.A., Buck K.W.;
RT "Complete nucleotide sequence of the infectious cloned DNA components
of tomato golden mosaic virus: potential coding regions and regulatory
sequences."
RL EMBO J. 3:2197-2205(1984).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
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EMBL; K02029; -; NOT_ANNOTATED_CDS.
PIR; A04170; Q0CVL1.
InterPro; IPR001191; Gemini_AL1.
Pfam; PF00799; Gemini_AL1; 1.
PRINTS; PR00227; GEMCOATALI.
ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 223 230 ATP (POTENTIAL).
SQ SEQUENCE 352 AA; 40332 MW; C33C938E9644B4A4 CRC64;

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Query Match 95.2%; Score 340; DB 1; Length 352;

Best Local Similarity 95.7%; Pred. No. 36-31;

Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 TLVWGFQVDSARGGCGTNSDAAAEALNASSKEEALQIREKTPKYLPAALNSNL 60
DB 111 TLVWGFQVDSARGGCGTNSDAAAEALNASSKEEALQIREKTPKYLFOFHLNSNL 170
QY 61 DRIFDKTPEP 70
DB 171 DRIFDKTPEP 180

```

##### RESULT 2

```

VAL1_PYMV
ID VAL1_PYMV STANDARD; PRT; 361 AA.
AC P27258;

```

```

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE A11 protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN SEQUENCE FROM N.A.
RP MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
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CC -----
CC EMBL; D00940; BAA00782.1; -.
CC InterPro; IPR001191; Geminini_AL1.
CC Pfam; PF00799; Geminini_AL1; 1.
CC PRINTS; PR00227; GEMCOATL1.
CC ProDom; PD000736; Geminini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;

Query Match 67.2%; Score 240; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 7.3e-20;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLFAFALNSNL 60
DB 110 TLVWGEFQVDRSARGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLFAFALNSNL 169
QY 61 DRIFDKTPE 69
DB 170 DRIFDKAPE 178

RESULT 3
VAL1 CLV1 CLV2 STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE A11 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN SEQUENCE FROM N.A.
RP Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA."
RL Nature 301:260-262(1983).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
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CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Geminini_AL1; 1.
KW ATP-binding.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753BE92D69 CRC64;

Query Match 63.6%; Score 227; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 2.2e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLFAFALNSNL 60
DB 109 TLVWGEFQVDRSARGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLFAFALNSNL 168
QY 61 DRIFDKTPE 70
DB 169 DRIFQEPAP 178

RESULT 4
VAL1 CLV1 CLV2 STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE A11 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN SEQUENCE FROM N.A.
RP MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain)."
RL Nucleic Acids Res. 18:197-198(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
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CC -----
CC EMBL; X17095; CAA34953.1; -.
CC InterPro; IPR001191; Geminini_AL1.
CC Pfam; PF00799; Geminini_AL1; 1.
CC PRINTS; PR00227; GEMCOATL1.
CC ProDom; PD000736; Geminini_AL1; 1.
KW ATP-binding.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16B80CB2D5E2C CRC64;

Query Match 63.6%; Score 227; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 2.2e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLFAFALNSNL 60
DB 109 TLVWGEFQVDRSARGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLFAFALNSNL 168
QY 61 DRIFDKTPE 70
DB 169 DRIFQEPAP 178

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RESULT 5
VAL1_TYLCV
ID VAL1_TYLCV STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AL1 protein (Cl protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36447;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93139778; PubMed=8423446;
RA Dry I.B., Rigden J.E., Krake L.R., Mullineaux P.M., Rezaian M.A.;
RT "Nucleotide sequence and genome organization of tomato leaf curl
  geminivirus.";
RL J. Gen. Virol. 74:147-151(1993).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR PIR; JQ1887; JQ1887.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
KW ATP-binding.
FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;

Query Match 61.6%; Score 220; DB 1; Length 362;
Best Local Similarity 52.9%; Pred. No. 1.4e-17; Indels 16; Gaps 1;
Matches 45; Conservative 9; Mismatches 15;

QY 1 TLVGEFQVDGRSARGGCGTSDNAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 60
DB 110 TLEWGFQIDGRSARGGCGTSDNAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 169
QY 61 DRI-----FKTPE 69
DB 170 DRIETPPLEVVYSPFLSSSFDRVPE 194

RESULT 6
VAL1_TYLCV
ID VAL1_TYLCV STANDARD; PRT; 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 protein (Cl protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Noris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
  from the west Mediterranean basin: the nucleotide sequence of an
  infectious clone from Spain.";
RL Arch. Virol. 135:165-170(1994).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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DR PIR; S22593; S22593.
DR PDB; 1L2M; 18-SEP-02.
DR PDB; 1L5I; 18-SEP-02.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding; 3D-structure.
FT NP_BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 40733 MW; 9717BAA07C93EFA7 CRC64;

Query Match 58.8%; Score 210; DB 1; Length 359;
Best Local Similarity 56.5%; Pred. No. 1.9e-16;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDGRSARGGCGTSDNAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 61
DB 111 LEWGTFFQIDGRSARGGCGTSDNAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 170

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CC EMBL; Z25751; CAA81026.1; -.
DR PIR; S39211; S39211.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 41065 MW; 2D170A51BF80A3EC CRC64;

Query Match 60.8%; Score 217; DB 1; Length 359;
Best Local Similarity 59.4%; Pred. No. 3e-17;
Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDGRSARGGCGTSDNAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 61
DB 111 LEWGTFFQIDGRSARGGCGTSDNAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 170
QY 62 RIFDKTPEP 70
DB 171 RVFQVPPAP 179

RESULT 7
VAL1_TYLCV
ID VAL1_TYLCV STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AL1 protein (Cl protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92107660; PubMed=1840676;
RA Kheyr-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
  Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a
  whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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DR EMBL; X61153; CAA43466.1; -.
DR PIR; S22593; S22593.
DR PDB; 1L2M; 18-SEP-02.
DR PDB; 1L5I; 18-SEP-02.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding; 3D-structure.
FT NP_BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 40733 MW; 9717BAA07C93EFA7 CRC64;

Query Match 58.8%; Score 210; DB 1; Length 359;
Best Local Similarity 56.5%; Pred. No. 1.9e-16;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVDGRSARGGCGTSDNAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 61
DB 111 LEWGTFFQIDGRSARGGCGTSDNAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 170

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QY 62 RIFDKTPEP 70
Db 171 KVQVPPAP 179

RESULT 8
VAL1 PHUV STANDARD; PRT; 349 AA.
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AL1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
RT comparison with bipartite geminiviruses.";
RL J. Gen. Virol. 74:2225-2231(1993).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC
CC EMBL; M10070; AAA46318.1; -
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 40190 MW; 80FA79DF6029A34 CRC64;

Query Match 57.1%; Score 204; DB 1; Length 353;
Best Local Similarity 57.1%; Pred. No. 8.8e-16;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGCOTSDAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 60
Db 110 TIEWGEFQVDSRGSGCOTSDAAAEALNASSKEALQIIREKIPEKYLFAFAALNSNL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFDKVPEP 179

RESULT 10
VAL1 ABMVV STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimmat G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC
CC EMBL; X15983; -; NOT_ANNOTATED_CDS.
CC PIR; A36214; QQCWML.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.

QY 62 RIFDKTPEP 70
Db 171 KVQVPPAP 179

RESULT 9
VAL1 BGWV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE AL1 protein (40.2 kDa protein).
GN AC1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]

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FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 355 AA; 40257 MW; 16A2CA8A63251E95 CRC64;

Query Match 56.9%; Score 203; DB 1; Length 355;
Best Local Similarity 55.7%; Pred. No. 1.2e-15;
Matches 39; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSGGCGTSDNDAARALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
Db 110 TAEWGFQIDGRSGRGCGQTANDSYAKALNAGDVQSALNHLKESQPKDYVLQHNIRSNL 169
Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAP 179

RESULT 11
VAL1_BCTV STANDARD; PRT; 358 AA.
AC P14931;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Ali protein (40.8 kDa protein).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
RT beet curly top virus."
RL EMBL J. 511761-1767(1986).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
CC EMBL; L14460; AAC32414.1; -.
CC PIR; JQ1870; JQ1870.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALI.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
KW NP_BIND 222 229 ATP (BY SIMILARITY).
FT NP_BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;

Query Match 56.0%; Score 200; DB 1; Length 358;
Best Local Similarity 52.9%; Pred. No. 2.5e-15;
Matches 37; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSGGCGTSDNDAARALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
Db 110 TAEWGFQIDGRSGRGCGQTANDSYAKALNAGDVQSALNHLKESQPKDYVLQHNIRSNL 169
Qy 61 DRIFDKTPEP 70
Db 170 QKIFQRPDP 179

RESULT 12
VAL1_TM0V STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Ali protein.

FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 355 AA; 40257 MW; 16A2CA8A63251E95 CRC64;

Query Match 56.9%; Score 203; DB 1; Length 355;
Best Local Similarity 55.7%; Pred. No. 1.2e-15;
Matches 39; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSGGCGTSDNDAARALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
Db 110 TAEWGFQIDGRSGRGCGQTANDSYAKALNAGDVQSALNHLKESQPKDYVLQHNIRSNL 169
Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAP 179

RESULT 13
VAL1_TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Ali protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN SEQUENCE FROM N.A.
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component."
RL Virology 185:151-161(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
CC EMBL; L14460; AAC32414.1; -.
CC PIR; JQ1870; JQ1870.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALI.
CC ProDom; PD000736; Gemini_AL1; 1.
CC ATP-binding.
KW NP_BIND 222 229 ATP (BY SIMILARITY).
FT NP_BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 8138B65CEAC6950 CRC64;

Query Match 56.0%; Score 200; DB 1; Length 361;
Best Local Similarity 52.9%; Pred. No. 2.6e-15;
Matches 37; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSGGCGTSDNDAARALNASSKEEALQIIREKIPEKYLFAFALNSNL 60
Db 110 TAEWGFQIDGRSGRGCGQTANDSYAKALNAGDVQSALNHLKESQPKDYVLQHNIRSNL 169
Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAP 179

RESULT 13
VAL1_TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Ali protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN SEQUENCE FROM N.A.
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component."
RL Virology 185:151-161(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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DR EMBL; X15656; CAA33688.1; -.
DR PIR; D40779; QOCVCI.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; I.
DR PRINTS; PR00227; GEMCOAT1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND. 219 226 ATP (POTENTIAL).
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match 53.5%; Score 191; DB 1; Length 357;
Best Local Similarity 62.3%; Pred. No. 2.7e-14;
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 4 WGEFQVGRSARGGCGTSDNDAAEALNASSKEALQIREKIPKYLFAFAALNSNLDRI 63
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
111 FGVSDIGRSARGGCGQANDAYAEALNSGSKSEALNLIKKEKAPKDYILQPHNLSNLDRI 170

Qy 64 F 64
Db 171 F 171

RESULT 14
ID VAL1_SLCV STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE AL1 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G.; Lardias I.B.;
RT Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype."
RL Virology 180:58-69(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
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CC
CC EMBL; M38183; AAC32410.1; ALT_INIT.
CC PIR; C36785; QOCVSI.
CC InterPro; IPR001191; Gemini AL1.
CC Pfam; PF00799; Gemini AL1; I.
CC PRINTS; PR00227; GEMCOAT1.
CC ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND. 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDAEBDD122110E CRC64;

Query Match 29.1%; Score 104; DB 1; Length 347;
Best Local Similarity 34.8%; Pred. No. 0.0002;
Matches 23; Conservative 14; Mismatches 25; Indels 4; Gaps 1;

Qy 5 GEFQVGRSARGGCGTSDNDAAEALNASSKEALQIREKIPKYLFAFAALNSNLDRI 64
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 GQYKVGSG----GSKSNKDDVTHNAVAGSAGEALDIKAGDKTFIVYHNLNLANVERLF 171

Qy 65 DKTEPE 70
Db 172 QKPEPE 177
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## RESULT 15

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TBL2_HUMAN
ID TBL2_HUMAN STANDARD; PRT; 447 AA.
AC Q3Y4F5; Q9U0E2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transducin beta-like 2 protein (WS beta-transducin repeats protein)
DE (WS-beta2TP) (Williams-Beuren syndrome chromosome region 13 protein).
GN TBL2 OR WBSCE13.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20044626; PubMed=10575226;
RA Perez Jurado L.A.; Wang Y.-K.; Francke U.; Cruces J.;
RT "TBL2, a novel transducin family member in the WBS deletion:
RT characterization of the complete sequence, genomic structure,
RT transcriptional variants and the mouse ortholog."
RL Cytogenet. Cell Genet. 86:277-284(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S.; Weil B.; Wellenreuther R.; Gassenhuber J.; Glassl S.;
RA Ansorge W.; Boecher M.; Bloecker H.; Bauersachs S.; Blum H.;
RA Lauber J.; Dueterhoeft A.; Beyer A.; Koehrer K.; Strack N.;
RA Mewes H.-W.; Ottenwelder B.; Obermaier B.; Tampe J.; Heubner D.;
RA Wambutt R.; Korn B.; Klein M.; Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs."
RL Genome Res. 11:422-435(2001).
RN [3]
RP SEQUENCE OF 14-447 FROM N.A.
RX MEDLINE=99075645; PubMed=9860302;
RA Meng X.; Lu X.; Li Z.; Green E.D.; Massa H.; Trask B.J.; Morris C.A.;
RA Keating M.T.;
RT "Complete physical map of the common deletion region in Williams
RT syndrome and identification and characterization of three novel
RT genes."
RL Hum. Genet. 103:590-599(1998).
CC -!- DISEASE: Haploinsufficiency of TBL2 may be the cause of certain
CC cardiovascular and musculo-skeletal abnormalities observed in
CC Williams-Beuren syndrome (WBS) [MIM:194050], a rare developmental
CC disorder. It is a contiguous gene deletion syndrome involving
CC genes from chromosome band 7q11.23.
CC -!- SIMILARITY: Contains 7 WD repeats.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF097484; AAF06823.1; -.
CC EMBL; AF097485; AAF06824.1; -.
CC EMBL; AF080162; CAB45751.1; -.
CC EMBL; AF056183; AAD28083.1; ALT_INIT.
CC PIR; T12544; T12544.
CC Genew; HGNC:11586; TBL2.
CC MIM; 605842; -.
CC MIM; 194050; -.
CC InterPro; IPR001680; WD40.
CC Pfam; PF00400; WD40; 5.
CC PRINTS; PR00320; GPROTEINBRPT.
CC ProDom; PD000018; WD40; 2.
CC SMART; SM00320; WD40; 5.
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DR PROSITE; PS00678; WD REPEATS 1; 1.  
DR PROSITE; PS00082; WD REPEATS 2; 3.  
DR PROSITE; PS0294; WD REPEATS\_REGION; 1.  
KW Repeat; WD repeat; Williams-Beuren syndrome.  
FT REPEAT 88 127 WD 1.  
FT REPEAT 134 174 WD 2.  
FT REPEAT 186 226 WD 3.  
FT REPEAT 228 267 WD 4.  
FT REPEAT 277 316 WD 5.  
FT REPEAT 329 367 WD 6.  
FT REPEAT 371 409 WD 7.  
SQ SEQUENCE 447 AA; 49797 MW; B260087ELA71D3F9 CRC64;  
  
Query Match 18.8%; Score 67; DB 1; Length 447;  
Best Local Similarity 32.1%; Pred.No. 4.3; Mismatches 23; Indels 4; Gaps 1;  
Matches 18; Conservative 11;  
  
QY 12 RSARGGCQTSDAAAEALNASSKEALQIIREKIPEKYLFAF---AALNSNLDRI 63  
Db 38 RSGRPACQKANGFPDPKSSGSKKQYQYQIRKEKPOQHNFTHRLAALKSHSGNI 93  
  
Search completed: December 23, 2003, 08:57:39  
Job time : 6.77778 secs







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SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;

Query Match 76.2%; Score 272; DB 12; Length 361;
Best Local Similarity 77.1%; Pred. No. 6.7e-24;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNLI 60
DB 111 TVWGEFQVDSRGSGGQTVNDAAAEALNAPDKRTALQIIREKIPEKYLFOFHNLSNLI 170
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QY 61 DRIFDKTPEP 70
DB 171 DRIFAKAPEP 180
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RESULT 6
Q67574 PRELIMINARY; PRT; 361 AA.
AC Q67574;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Putative replicative protein.
GN ALI.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales P.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration.";
RL Phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RT "Differentiation of bean-infecting geminiviruses by nucleic acid
RT hybridization probes and aspects of bean golden mosaic in Brazil.";
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus.";
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
RL EMBL; M88686; AAA46312.1; -.
DR InterPro: IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini AL1; 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 75.6%; Score 270; DB 12; Length 361;
Best Local Similarity 76.1%; Pred. No. 2e-23;
Matches 51; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 4 WGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNLI 63
DB 113 WGEFQVDSRGSGGQTDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLI 172
|||||
QY 64 FDKTPEP 70
DB 173 FTKAPDP 179
|||||

RESULT 7
Q9QDB1 PRELIMINARY; PRT; 225 AA.
AC Q9QDB1;
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DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Cowpea golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGMV-BR;
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RT Brazil.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF198708; AAF06318.1; -.
DR InterPro: IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini AL1; 1.
FT NON_TER 225
SQ SEQUENCE 225 AA; 25766 MW; 1089C86BD8D15B5D CRC64;

Query Match 75.1%; Score 268; DB 12; Length 225;
Best Local Similarity 76.1%; Pred. No. 2e-23;
Matches 51; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 4 WGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNLI 63
DB 113 WGEFQVDSRGSGGQTDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLI 172
|||||
QY 64 FDKTPEP 70
DB 173 FKKEPEP 179
|||||

RESULT 8
Q9ELT8 PRELIMINARY; PRT; 314 AA.
AC Q9ELT8;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Replication associated protein.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288237; AAG01006.1; -.
DR InterPro: IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini AL1; 1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 75.1%; Score 268; DB 12; Length 314;
Best Local Similarity 79.4%; Pred. No. 2.9e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFAFAALNSNLI 60
DB 110 TITWGEFQVDSRGSGGQTDAAAEALNAGSKEEALQIIREKIPEKYLFOFHNLSNLI 169
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Qy 61 DRIFDKTP 68
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Db 170 DRIFSPPP 177

RESULT 9
Q9QS55 PRELIMINARY; PRT; 364 AA.
AC Q9QS55;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Vaiverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Vaiverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RT virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0(1999).
DR EMBL; AF104036; AAD47173.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D5E CRC64;

Query Match 75.1%; Score 268; DB 12; Length 364;
Best Local Similarity 79.4%; Pred. No. 3.5e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 TLWGEFQVDRSGRGCGQTSNDAAAEALNASSKEALQIIREKIPKYLFAFALNSNL 60
    : |||||
Db 110 TIWGEFQVDRSGRGCGQQTANDAAAEALNASSKEALQIIREKIPKYLFAFALNSNL 169
    : |||||

Qy 61 DRIFDKTP 68
    |||||
Db 170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Jamaica;
RA Roye M.E., McLaughlin W.A., Nakha N.K., Maxwell D.P.;
RT "Genetic Diversity among geminiviruses associated with the weed
RT species Sida spp, Macroptilium lathyroides, and Wissadula amplissima
RT from Jamaica.";
RL Plant Dis. 81:1251-1258(1997).
DR EMBL; U67926; AAB97865.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.

DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D5E CRC64;

Query Match 73.1%; Score 261; DB 12; Length 235;
Best Local Similarity 73.1%; Pred. No. 1.4e-22;
Matches 49; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 4 WGEFQVDRSGRGCGQTSNDAAAEALNASSKEALQIIREKIPKYLFAFALNSNL 63
    : |||||
Db 113 WGIFQIDGRSARGCGQQTANDAAAEALNASSKEALQIIREKIPKYLFAFALNSNL 172
    : |||||

Qy 64 FKTPPEP 70
    |||||
Db 173 FTKAPDP 179

RESULT 11
Q8QPU4 PRELIMINARY; PRT; 235 AA.
AC Q8QPU4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG-Bil;
RA Ribeiro S.G., Ambrozecivius L.P., de Avila A.C., Calegario R.P.,
RA Fernandes J.J., Lima M.P., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049208; AAL82833.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BE0DD9C810 CRC64;

Query Match 73.1%; Score 261; DB 12; Length 235;
Best Local Similarity 73.1%; Pred. No. 1.4e-22;
Matches 49; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 4 WGEFQVDRSGRGCGQTSNDAAAEALNASSKEALQIIREKIPKYLFAFALNSNL 63
    : |||||
Db 113 WGIFQIDGRSARGCGQQTANDAAAEALNASSKEALQIIREKIPKYLFAFALNSNL 172
    : |||||

Qy 64 FKTPPEP 70
    |||||
Db 173 FTKAPDP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;
```

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RN
RC SEQUENCE FROM N.A.
RP ROYAL M.E.;
RA STRAIN=Jamaican;
RL Thesis (1996), Biochemistry, University of the West Indies, Jamaica.
RR EMBL: U75278; AAB36919.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR PRODOM; PD000736; Gemini_AL1; 1.
FT NON TER      1
FT              149
FT              149
SQ SEQUENCE      149 AA; 16785 MW; B4CF5EED4C9CD508 CRC64;

Query Match          72.0%; Score 257; DB 12; Length 149;
Best Local Similarity 68.6%; Pred.No. 2.4e-22;
Matches 48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGFBQVDGRARGGCOTSDNDAAEALNASKEKRALQIIRKIPKYLFAPFAALNSNL 60
   :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 52 TIWGVFQIDGRARGGCQTSDNDAAEALNSGTKEAAMRIVKEKLPEKFLFYQHNLSSNL 111
   :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 61 DRIFDKTPEP 70
   |||||::|||
Db 112 DRIFMKDPEP 121

RESULT 15
QNYLA4
ID QNYLA4 PRELIMINARY; PRT; 233 AA.
AC QNYLA4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica strain 1;
RC ROYAL M.E.;
RR "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica."
RT Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Jamaica strain 1;
RA ROYAL M.E., McLaughlin W.A., Maxwell D.P.;
RR "Molecular characterization of two distinct geminiviruses infecting M. lathyrus from Jamaica."
RT Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AF098940; AAD17850.1; -
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR PRODOM; PD000736; Gemini_AL1; 1.
FT NON TER      233
FT              233
SQ SEQUENCE      233 AA; 26356 MW; AA490AF4D2166A02 CRC64;

Query Match          72.0%; Score 257; DB 12; Length 233;
Best Local Similarity 68.6%; Pred.No. 4e-22;
Matches 48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGFBQVDGRARGGCOTSDNDAAEALNASKEKRALQIIRKIPKYLFAPFAALNSNL 60
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Db 110 TIWGVFQIDGRARGGCQTSDNDAAEALNSGTKEAAMRIVKEKLPEKFLFYQHNLSSNL 169
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QY 61 DRIFDKTPEP 70
   |||||::|||
Db 170 DRIFMKDPEP 179

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Search completed: December 23, 2003, 09:03:36  
Job time : 26.3333 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds  
(without alignments)  
340.128 Million cell updates/sec

Title: US-09-289-346B-7

Perfect score: 359

Sequence: 1 TLVWGFQVDRSARGCQT.....FOFHNLNSALAAIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359	100.0	70	21	AA186683
2	342	95.3	70	21	AA186677
3	342	95.3	356	21	AA186687
4	334	93.0	70	21	AA186685
5	331	92.2	70	21	AA186688
6	330	91.9	70	21	AA186692
7	328	91.4	70	21	AA186684
8	328	91.4	70	21	AA186690
9	327	91.1	70	21	AA186678
					Mutant peptide der
					Peptide fragment f
					Amino acid sequenc
					Mutant peptide der
					Mutant peptide der
					Mutant peptide der
					Mutant peptide der
					Mutant peptide der
					Mutant peptide der

10	327	91.1	70	21	AA186686	Mutant peptide der
11	326	90.8	70	21	AA186699	Mutant peptide der
12	324	90.3	70	21	AA186680	Mutant peptide der
13	324	90.3	70	21	AA186691	Mutant peptide der
14	321	89.4	70	21	AA186681	Mutant peptide der
15	318	88.6	70	21	AA186682	Mutant peptide der
16	310	86.4	70	21	AA186679	Mutant peptide der
17	213	59.3	353	18	AAW34338	Bean golden mosaic
18	213	59.3	353	18	AAW34332	Bean golden mosaic
19	213	59.3	353	18	AAW34333	Bean golden mosaic
20	213	59.3	353	18	AAW34334	Bean golden mosaic
21	213	59.3	353	18	AAW34335	Bean golden mosaic
22	211	58.8	353	8	AAW70407	ORF 4 gene product
23	211	58.8	359	17	AAW88870	Sardinian tomato Y
24	211	58.8	359	17	AAW88871	Sardinian tomato Y
25	211	58.8	359	17	AAW88872	Sardinian tomato Y
26	211	58.8	361	18	AAW34336	Tomato mottle viru
27	211	58.8	361	18	AAW34324	Tomato mottle viru
28	211	58.8	361	18	AAW34325	Tomato mottle viru
29	211	58.8	361	18	AAW34326	Tomato mottle viru
30	208.5	58.1	361	8	AAW70562	Product of ORF 4 f
31	201.5	56.1	50	23	AAO22043	Retinoblastoma-bin
32	194	54.0	362	19	AAW56495	Tobacco leaf curl
33	193	53.8	357	18	AAW34329	Tomato yellow leaf
34	193	53.8	357	18	AAW34330	Tomato yellow leaf
35	193	53.8	357	18	AAW34331	Tomato yellow leaf
36	185	51.5	357	18	AAW34337	Tomato yellow leaf
37	104	29.0	142	24	ABP58120	Tomato yellow leaf
38	68	18.9	447	21	AAW9659	Human GTPase assoc
39	68	18.9	447	21	AAW87089	Human secreted pro
40	68	18.9	447	21	AAW6744	Membrane-bound pro
41	68	18.9	447	21	AAW50947	Human adult aorta
42	68	18.9	447	22	AAU29150	Human PKO polypept
43	68	18.9	447	22	AAW3267	Human polypeptide,
44	68	18.9	447	22	AAW3267	Human gene 26 enco
45	68	18.9	447	22	AAW65267	Human PRO1125 (UNQ

#### ALIGNMENTS

#### RESULT 1

AA186683

ID AA186683 standard; peptide; 70 AA.

AC AA186683;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
XX Gemini virus; replication protein; Rep protein; AL1; transgenic plant;  
KW ribosome binding region; resistance; geminivirus infection.

OS Synthetic.

OS Tomato golden mosaic virus.

Key Location/Qualifiers

FT Misc-difference 59 /note= "wild type residue replaced with Ala"

FT Misc-difference 61 /note= "wild type residue replaced with Ala"

FT Misc-difference 62 /note= "wild type residue replaced with Ala"

FT Misc-difference 62 /note= "wild type residue replaced with Ala"

FT Misc-difference 62 /note= "wild type residue replaced with Ala"

XX WO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Claim 53; Page 45; 73pp; English.  
 XX The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX Sequence 70 AA;  
 SQ Query Match 100.0%; Score 359; DB 21; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 1e-38;  
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVQGRSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLQFHNLSAL 60  
 DB 1 TLVWGEFQVQGRSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLQFHNLSAL 60  
 QY 61 AAIFDKTPEP 70  
 DB 61 AAIFDKTPEP 70  
 RESULT 2  
 AAB18677  
 ID AAB18677 standard; peptide; 70 AA.  
 AC AAB18677;  
 XX 22-JAN-2001 (first entry)  
 XX Peptide fragment from Rep protein of TGMV (amino acids 110-179).  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.  
 XX Tomato golden mosaic virus.  
 XX WO200054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.  
 XX 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 PT Transgenic plants with increased resistance to geminivirus infection

XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Disclosure; Page 18; 73pp; English.  
 XX The present sequence is derived from a geminivirus replication (Rep)  
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,  
 CC catalyzes cleavage and ligation of single-stranded DNA, and interacts  
 CC with other viral and host proteins. Mutants of the AL1 protein are used  
 CC to produce transgenic plants. The mutation in AL1 is present in a  
 CC ribosome binding region, and expression of mutant AL1 protein imparts  
 CC increased resistance to geminivirus infection in the plant. Mutant AL1  
 CC proteins are useful for producing plants having increased resistance or  
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,  
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl  
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato  
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,  
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or  
 CC beet curly top virus.  
 XX Sequence 70 AA;  
 SQ Query Match 95.3%; Score 342; DB 21; Length 70;  
 Best Local Similarity 95.7%; Pred. No. 1.6e-36;  
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVQGRSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLQFHNLSAL 60  
 DB 1 TLVWGEFQVQGRSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLQFHNLSAL 60  
 QY 61 AAIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 3  
 AAB18687  
 ID AAB18687 standard; peptide; 356 AA.  
 AC AAB18687;  
 XX 22-JAN-2001 (first entry)  
 XX Amino acid sequence of a geminivirus replication protein of TGMV.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.  
 XX Tomato golden mosaic virus.  
 XX Key Location/Qualifiers  
 FT Misc-difference 354 /note= "unspecified amino acid"  
 FT WO200054573-A1.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.  
 XX 09-APR-1999; 99US-0289346.  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 PT Transgenic plants with increased resistance to geminivirus infection



PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX -

XX Disclosure; Page 47-48; 73pp; English.

XX The present sequence represents a geminivirus replication (Rep)  
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,  
 CC catalyses cleavage and ligation of single-stranded DNA, and interacts  
 CC with other viral and host proteins. Mutants of the AL1 protein are used  
 CC to produce transgenic plants. The mutation in AL1 is present in a  
 CC ribosome binding region, and expression of mutant AL1 protein imparts  
 CC increased resistance to geminivirus infection in the plant. Mutant AL1  
 CC proteins are useful for producing plants having increased resistance or  
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,  
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl  
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato  
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,  
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or  
 CC beet curly top virus.

XX Sequence 356 AA;

Query Match 95.3%; Score 342; DB 21; Length 356;  
 Best Local Similarity 95.7%; Pred. No. 1.3e-35;  
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSRGSGCQTSDNDAALNASSKEALQIIRKIPKYLQFPHNLSAL 60  
 Db 110 TLVWGFQVDSRGSGCQTSDNDAALNASSKEALQIIRKIPKYLQFPHNLSNL 169

QY 61 AAIFDKTPEP 70  
 Db 170 DRIFDKTPEP 179

RESULT 4

AA18685  
 ID AAB18685 standard; peptide; 70 AA.

XX AAB18685;

XX 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.

XX Synthetic.  
 XX Tomato golden mosaic virus.

XX Key Location/Qualifiers  
 FH Misc-difference 10  
 FT /note= "wild type residue replaced with Ala"

XX WO200054573-Al.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence

PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Claim 53; Page 46; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA;

Query Match 93.0%; Score 334; DB 21; Length 70;  
 Best Local Similarity 94.3%; Pred. No. 1.8e-35;  
 Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSRGSGCQTSDNDAALNASSKEALQIIRKIPKYLQFPHNLSAL 60  
 Db 1 TLVWGFQVDSRGSGCQTSDNDAALNASSKEALQIIRKIPKYLQFPHNLSNL 60

QY 61 AAIFDKTPEP 70

Db 61 DRIFDKTPEP 70

RESULT 5

AA18688  
 ID AAB18688 standard; peptide; 70 AA.

XX AAB18688;

XX 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

XX Tomato golden mosaic virus.

XX Key Location/Qualifiers  
 FH Misc-difference 19  
 FT /note= "wild type residue replaced with Ala"

XX Misc-difference 20

XX /note= "wild type residue replaced with Ala"

XX WO200054573-Al.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection  
 PT

PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX -  
 XX  
 PS Disclosure; Page 48; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;

Query Match 92.2%; Score 331; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 4.3e-35;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVGRSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60  
 DB 1 TLVWGEFQVGRSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60  
 QY 61 AAIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70

RESULT 6  
 AAB18692  
 ID AAB18692 standard; peptide; 70 AA.  
 AC AAB18692;  
 XX  
 XX  
 DT 22-JAN-2001 (first entry)  
 XX  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX  
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 66 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 69 /note= "wild type residue replaced with Ala"  
 FT  
 XX  
 XX WO200054573-Al.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 15-MAR-2000; 2000WO-US06759.  
 XX  
 PR 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 DR

PT Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX -  
 XX  
 PS Disclosure; Page 50; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 SQ Sequence 70 AA;

Query Match 91.9%; Score 330; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 5.9e-35;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TLVWGEFQVGRSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60  
 DB 1 TLVWGEFQVGRSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60  
 QY 61 AAIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70

RESULT 7  
 AAB18684  
 ID AAB18684 standard; peptide; 70 AA.  
 AC AAB18684;  
 XX  
 XX  
 DT 22-JAN-2001 (first entry)  
 XX  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX  
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 OS Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 7 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"  
 FT  
 XX  
 XX WO200054573-Al.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 15-MAR-2000; 2000WO-US06759.  
 XX  
 PR 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 DR

XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant All protein with a mutation in the Rb binding region  
 PT  
 XX  
 PS  
 PS Claim 52; Page 45; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as All. All binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the All  
 CC protein are used to produce transgenic plants. The mutation in All is  
 CC present in a ribosome binding region, and expression of mutant All  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant All proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 XX Sequence 70 AA;

Query Match 91.4%; Score 328; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 1.1e-34;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGQTSNDAAALNASSKEKALQIIREKIPEKYLFOFHNLSAL 60  
 Db 1 TLVWGEAANDGRSGRGCGQTSNDAAALNASSKEKALQIIREKIPEKYLFOFHNLSNL 60

QY 61 AAIFDKTPEP 70  
 Db 61 DRIFDKTPEP 70

RESULT 8  
 AAB18690  
 ID AAB18690 standard; peptide; 70 AA.

AC AAB18690;  
 XX  
 DT 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (All) protein.  
 DE Geminivirus; replication protein; Rep protein; All; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.

XX Synthetic.  
 OS Tomato golden mosaic virus.

XX Key Location/Qualifiers  
 FH Misc-difference 27 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 30 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 30 /note= "wild type residue replaced with Ala"

XX WO2000054573-Al.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYN-C-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX

DR WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant All protein with a mutation in the Rb binding region  
 PT  
 XX  
 PS  
 PS Disclosure; Page 49; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as All. All binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the All  
 CC protein are used to produce transgenic plants. The mutation in All is  
 CC present in a ribosome binding region, and expression of mutant All  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant All proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA;

Query Match 91.4%; Score 328; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 1.1e-34;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGQTSNDAAALNASSKEKALQIIREKIPEKYLFOFHNLSAL 60  
 Db 1 TLVWGEAANDGRSGRGCGQTSNDAAALNASSKEKALQIIREKIPEKYLFOFHNLSNL 60

QY 61 AAIFDKTPEP 70  
 Db 61 DRIFDKTPEP 70

RESULT 9  
 AAB18678

ID AAB18678 standard; peptide; 70 AA.

AC AAB18678;

XX  
 DT 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (All) protein.  
 DE Geminivirus; replication protein; Rep protein; All; transgenic plant;  
 XX ribosome binding region; resistance; geminivirus infection.

XX Synthetic.  
 OS Tomato golden mosaic virus.

XX Key Location/Qualifiers  
 FH Misc-difference 12 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 13 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 15 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 15 /note= "wild type residue replaced with Ala"

XX WO2000054573-Al.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYN-C-) UNIV NORTH CAROLINA STATE.

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XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX XX WPI; 2000-618851/59.
XX DR
XX XX Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX FT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT
XX PS Claim 53; Page 42-43; 73pp; English.
XX XX
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 91.1%; Score 327; DB 21; Length 70;
Best Local Similarity 91.4%; Pred No. 1.4e-34;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 TLVNGEFQVQGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
Db 1 TLVNGEFQVQGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
Qy 61 AAIEDKTPPEP 70
Db 61 DRIFDKTPPEP 70
RESULT 10
AAB18686
ID AAB18686 standard; peptide; 70 AA.
AC AAB18686;
XX DT
XX DT 22-JAN-2001 (first entry)
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX XX
XX XX Key Location/Qualifiers
XX FT Misc-difference 24 /note= "wild type residue replaced with Leu"
XX FT Misc-difference 25 /note= "wild type residue replaced with Leu"
XX FT Misc-difference 26 /note= "wild type residue replaced with Leu"
XX FT Misc-difference 26 /note= "wild type residue replaced with Leu"
XX PN WO200054573-A1.
XX XX
XX PD 21-SEP-2000.
XX XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX XX
XX PR 18-MAR-1999; 99US-0125004.

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PR 09-APR-1999; 99US-0289346.
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX XX
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX XX WPI; 2000-618851/59.
XX DR
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PT
XX PS Claim 53; Page 46; 73pp; English.
XX XX
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 91.1%; Score 327; DB 21; Length 70;
Best Local Similarity 91.4%; Pred No. 1.4e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 TLVNGEFQVQGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
Db 1 TLVNGEFQVQGRSARGGQTSNDLLLEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Qy 61 AAIEDKTPPEP 70
Db 61 DRIFDKTPPEP 70
RESULT 11
AAB18689
ID AAB18689 standard; peptide; 70 AA.
AC AAB18689;
XX DT
XX DT 22-JAN-2001 (first entry)
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX XX
XX XX Key Location/Qualifiers
XX FT Misc-difference 22 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX PN WO200054573-A1.
XX XX
XX PD 21-SEP-2000.
XX XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX XX

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```

PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
DR WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
FT comprise a nucleic acid construct containing a nucleic acid sequence
FT encoding a mutant AL1 protein with a mutation in the Rb binding region
FT
PS Disclosure; Page 48-49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, bean dwarf mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 90.8%; Score 326; DB 21; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.9e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDRSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLFOFHNLSAL 60
DB 1 TLVWGEFQVDRSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLFOFHNLSAL 60
QY 61 AAFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 12
AAB18680
ID AAB18680 standard; peptide; 70 AA.
XX
AC AAB18680;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
OS Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 42 /note= "wild type residue replaced with Ala"
FT Misc-difference 43 /note= "wild type residue replaced with Ala"
FT Misc-difference 44 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-Al.
XX
PD 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
FT comprise a nucleic acid construct containing a nucleic acid sequence
FT encoding a mutant AL1 protein with a mutation in the Rb binding region
FT
PS Claim 52; Page 43-44; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, bean dwarf mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 90.3%; Score 324; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 3.5e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 TLVWGEFQVDRSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLFOFHNLSAL 60
DB 1 TLVWGEFQVDRSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLFOFHNLSAL 60
QY 61 AAFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 13
AAB18691
ID AAB18691 standard; peptide; 70 AA.
XX
AC AAB18691;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
OS Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 34 /note= "wild type residue replaced with Ala"
FT Misc-difference 35 /note= "wild type residue replaced with Ala"
FT Misc-difference 36 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-Al.
XX
PD 21-SEP-2000.

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PN WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Disclosure; Page 49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 90.3%; Score 324; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 3.5e-34;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
XX 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
XX
XX 61 AAIFDKTPEP 70
XX 61 DRIFDKTPEP 70
XX
XX RESULT 14
XX AAB18681
XX ID AAB18681 standard; peptide; 70 AA.
XX AC AAB18681;
XX XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 47
XX FT /note= "wild type residue replaced with Ala"
XX FT Misc-difference 48
XX FT /note= "wild type residue replaced with Ala"
XX FT

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FT Misc-difference 49
FT /note= "wild type residue replaced with Ala"
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XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 52; Page 44; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
XX
XX Query Match 89.4%; Score 321; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 8.6e-34;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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XX 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
XX 1 TLVWGEFQVDSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
XX
XX 61 AAIFDKTPEP 70
XX 61 DRIFDKTPEP 70
XX
XX RESULT 15
XX AAB18682
XX ID AAB18682 standard; peptide; 70 AA.
XX AC AAB18682;
XX XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 52
XX FT

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FT Misc-difference 54 /note= "wild type residue replaced with Ala"  
 FT /note= "wild type residue replaced with Ala"  
 FT Misc-difference 55 /note= "wild type residue replaced with Ala"  
 FT /note= "wild type residue replaced with Ala"  
 XX WO200054573-A1.  
 PN  
 XX  
 XX PD 21-SEP-2000.  
 XX  
 XX PF 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX PR 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX  
 XX PA (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX PI Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX  
 XX DR WPI; 2000-618851/59.  
 XX

Transgenic plants with increased resistance to geminivirus infection  
 comprise a nucleic acid construct containing a nucleic acid sequence  
 encoding a mutant AL1 protein with a mutation in the Rb binding region  
 \_

Claim 53; Page 44-45; 73pp; English.

The present sequence represents a mutant peptide, derived from a  
 geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 protein are used to produce transgenic plants. The mutation in AL1 is  
 present in a ribosome binding region, and expression of mutant AL1  
 protein imparts increased resistance to geminivirus infection in the  
 plant. Mutant AL1 proteins are useful for producing plants having  
 increased resistance or reduced sensitivity to a geminivirus such as  
 tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 virus, cotton leaf curl virus or beet curly top virus.

SQ Sequence 70 AA;

Query Match 88.6%; Score 318; DB 21; Length 70;  
 Best Local Similarity 91.4%; Pred. No. 2.1e-33;  
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVGRSARGGQTSNDAAAEALNASSKEEALQIREKIPKYLFOFHNLSAL 60  
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 Db 1 TLVWGEFQVGRSARGGQTSNDAAAEALNASSKEEALQIREKIPKYLFOFHNLSAL 60  
 |||||

QY 61 AAIFDKTPEP 70  
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 Db 61 DRIFDKTPEP 70  
 |||||

Search completed: December 23, 2003, 08:56:30  
 Job time : 32.6667 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 11.6667 Seconds  
(without alignments)  
253.865 Million cell updates/sec

Title: US-09-289-346B-7

Perfect score: 359

Sequence: 1 TLVWGFQVDSARGGCQT.....FOHNLNSALAAIFDKTEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*
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- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	213	59.3	353	3	US-08-838-151A-44
2	213	59.3	353	3	US-08-838-151A-46
3	213	59.3	353	3	US-08-838-151A-49
4	213	59.3	353	3	US-08-838-151A-52
5	213	59.3	353	3	US-08-838-151A-55
6	211	58.8	359	3	US-08-809-103B-2
7	211	58.8	359	3	US-08-809-103B-4
8	211	58.8	359	3	US-08-809-103B-6
9	211	58.8	359	3	US-08-809-103B-8
10	211	58.8	361	3	US-08-838-151A-2
11	211	58.8	361	3	US-08-838-151A-4
12	211	58.8	361	3	US-08-838-151A-6
13	211	58.8	361	3	US-08-838-151A-8
14	193	53.8	357	3	US-08-838-151A-24
15	193	53.8	357	3	US-08-838-151A-27
16	193	53.8	357	3	US-08-838-151A-30
17	185	51.5	357	3	US-08-838-151A-20
18	68	18.9	447	4	US-09-996-243-369
19	68	18.9	447	4	US-09-482-273-128
20	68	18.9	447	4	US-09-482-273-229
21	63.5	17.7	244	4	US-09-328-352-4541
22	63.5	17.7	2161	1	US-07-745-206A-2
23	63.5	17.7	2161	1	US-08-455-543A-49
24	63.5	17.7	2161	1	US-08-455-543A-51
25	63.5	17.7	2161	2	US-08-233-305C-49
26	63.5	17.7	2161	2	US-08-233-305C-51
27	63.5	17.7	2161	2	US-08-311-363-2

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Sequence 34, Appli  
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Sequence 27, Appli  
Sequence 28, Appli  
Sequence 29, Appli  
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Sequence 5120, Ap  
Sequence 4834, Ap  
Sequence 20895, A  
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Patent No. 5422248

28 62.5 17.4 512 4 US-09-319-588C-4  
29 60.5 16.9 131 3 US-08-838-151A-14  
30 59 16.4 293 4 US-09-414-276-3  
31 59 16.4 335 4 US-09-414-276-6  
32 59 16.4 531 4 US-08-976-063E-34  
33 58 16.2 374 2 US-08-928-892-51  
34 58 16.2 374 4 US-09-339-972-51  
35 57 15.9 454 3 US-08-446-100-26  
36 57 15.9 454 3 US-08-446-100-27  
37 57 15.9 454 3 US-08-446-100-28  
38 57 15.9 454 3 US-08-446-100-29  
39 57 15.9 454 3 US-08-446-100-30  
40 56.5 15.7 322 4 US-09-134-001C-5120  
41 56.5 15.7 707 4 US-09-328-352-4834  
42 56 15.6 290 4 US-09-252-991A-20895  
43 56 15.6 602 2 US-08-419-852-6  
44 56 15.6 771 1 US-07-923-976-6  
45 56 15.6 783 6 5422248-2

ALIGNMENTS

RESULT 1  
US-08-838-151A-44  
; Sequence 44, Application US/08838151A  
; Patent No. 6291743  
; GENERAL INFORMATION:  
; APPLICANT: Stout, John T  
; APPLICANT: Luu, Hang T  
; APPLICANT: Maxwell, Douglas  
; APPLICANT: Ahlquist, Paul  
; APPLICANT: Hanson, Steve  
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
; TITLE OF INVENTION: Genes  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
; STREET: Two Prudential Plaza, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838,151A  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mueller, Lisa V  
; REGISTRATION NUMBER: 38,978  
; REFERENCE/DOCKET NUMBER: SVS3801P0260  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-616-5400  
; TELEFAX: 312-616-5460  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 353 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-838-151A-44

Query Match 59.3%; Score 213; DB 3; Length 353;

Best Local Similarity 58.6%; Pred. No. 7, 9e-21;

Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGGCQTSDNDAABAINASSKEALQIREKIPKYLQFHNLSAL 60



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Db      110 TIWGGFQVDRSGRGCGCOTSDAAAEALNASKKEALQIIRKIPKYLQFPHNLSAL 169
Qy      61 AAIFDKTPEP 70
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Db      170 ERIFVKVPEP 179

RESULT 2
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; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

Query Match      59.3%; Score 213; DB 3; Length 353;
Best Local Similarity 58.6%; Pred. No. 7.9e-21;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy      1 TLVWGFQVDRSGRGCGCOTSDAAAEALNASKKEALQIIRKIPKYLQFPHNLSAL 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      110 TIWGGFQVDRSGRGCGCOTSDAAAEALNASKKEALQIIRKIPKYLQFPHNLSAL 169

Qy      61 AAIFDKTPEP 70
        ||| |||
Db      170 ERIFVKVPEP 179

RESULT 3
US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul

```

```

; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-49

Query Match      59.3%; Score 213; DB 3; Length 353;
Best Local Similarity 58.6%; Pred. No. 7.9e-21;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy      1 TLVWGFQVDRSGRGCGCOTSDAAAEALNASKKEALQIIRKIPKYLQFPHNLSAL 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      110 TIWGGFQVDRSGRGCGCOTSDAAAEALNASKKEALQIIRKIPKYLQFPHNLSAL 169

Qy      61 AAIFDKTPEP 70
        ||| |||
Db      170 ERIFVKVPEP 179

RESULT 4
US-08-838-151A-52
; Sequence 52, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

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```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-52

Query Match 59.3%; Score 213; DB 3; Length 353;
Best Local Similarity 58.6%; Pred. No. 7.9e-21;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGGCGTSDAAEALNASSKEALQIIRKIPKYLQFHNLSAL 60
   |||||
Db 110 TIWGFQVDGRSARGGCGTSDAAEALNASSKEALQIIRKIPKYLQFHNLSAL 60
   |||||

QY 61 AAIPTKTPPEP 70
   |||||
Db 170 ERIFVKVPEP 179
   |||||

```

```

RESULT 5
US-08-838-151A-55
; Sequence 55, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; US-08-838-151A-55

Query Match 59.3%; Score 213; DB 3; Length 353;
Best Local Similarity 58.6%; Pred. No. 7.9e-21;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGFQVDGRSARGGCGTSDAAEALNASSKEALQIIRKIPKYLQFHNLSAL 60
   |||||
Db 110 TIWGFQVDGRSARGGCGTSDAAEALNASSKEALQIIRKIPKYLQFHNLSAL 60
   |||||

QY 61 AAIPTKTPPEP 70
   |||||
Db 170 ERIFVKVPEP 179
   |||||

RESULT 6
US-08-809-103B-2
; Sequence 2, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-2

Query Match 58.8%; Score 211; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 1.5e-20;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVWGFQVDGRSARGGCGTSDAAEALNASSKEALQIIRKIPKYLQFHNLSALA 61
   |||||
Db 111 LEWGFQVDGRSARGGCGTSDAAEALNASSKEALQIIRKIPKYLQFHNLSALA 61
   |||||

QY 62 AAIPTKTPPEP 70
   |||||

```

Db 171 KVFQVPPAP 179

# RESULT 7

US-08-809-103B-4  
 ; Sequence 4, Application US/08809103B  
 ; Patent No. 6133505  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GRONENBORN, Bruno  
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND METHODS FOR OBTAINING SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: YOUNG & THOMPSON  
 ; STREET: 745 South 23rd Street  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; COUNTRY: U.S.A.  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/809,103B  
 ; FILING DATE: 17-MAR-1997  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: FR 94.11040  
 ; FILING DATE: 15-SEP-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/FR95/01192  
 ; FILING DATE: 15-SEP-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: PATCH, Andrew J.  
 ; REGISTRATION NUMBER: 32,925  
 ; REFERENCE/DOCKET NUMBER: US94AL CNR TOM  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 521-2297  
 ; TELEFAX: (703) 685-0573  
 ; TELEX: 248425 EMBON  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 359 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-809-103B-4

Query Match 58.8%; Score 211; DB 3; Length 359;

Best Local Similarity 56.5%; Pred. No. 1.5e-20;  
 Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVNGEFQVDRGARGCQTSNDAAALNASSKEALQIIREKIPEKYLFOPHNLSALA 61  
 Db 111 LEWGTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNINSNLD 170

QY 62 AIFDKTPEP 70

Db 171 KVFQVPPAP 179

# RESULT 8

US-08-809-103B-6  
 ; Sequence 6, Application US/08809103B  
 ; Patent No. 6133505  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GRONENBORN, Bruno  
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND METHODS FOR OBTAINING SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: YOUNG & THOMPSON  
 STREET: 745 South 23rd Street  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/809,103B  
 FILING DATE: 17-MAR-1997  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 94.11040  
 FILING DATE: 15-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/FR95/01192  
 FILING DATE: 15-SEP-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PATCH, Andrew J.  
 REGISTRATION NUMBER: 32,925  
 REFERENCE/DOCKET NUMBER: US94AL CNR TOM  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 521-2297  
 TELEFAX: (703) 685-0573  
 TELEX: 248425 EMBON  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 359 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-809-103B-6

Query Match 58.8%; Score 211; DB 3; Length 359;

Best Local Similarity 56.5%; Pred. No. 1.5e-20;  
 Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVNGEFQVDRGARGCQTSNDAAALNASSKEALQIIREKIPEKYLFOPHNLSALA 61  
 Db 111 LEWGTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNINSNLD 170

QY 62 AIFDKTPEP 70

Db 171 KVFQVPPAP 179

# RESULT 9

US-08-809-103B-8  
 ; Sequence 8, Application US/08809103B  
 ; Patent No. 6133505  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GRONENBORN, Bruno  
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND METHODS FOR OBTAINING SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: YOUNG & THOMPSON  
 ; STREET: 745 South 23rd Street  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; COUNTRY: U.S.A.  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/809,103B

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; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8

Query Match 58.8%; Score 211; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 1.5e-20;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVWGEFQVDSRGSGGQTSNDAAALNASSKEEALQIIRKIPKYLFPQHNLNSALA 61
Db 111 LWTGDFQIDGRSARGGQQTNDAYAKAINAGSKQALDVIKELAPRDYVLHFNINSLD 170

QY 62 AIFDKTPEP 70
Db 171 KVFOVPPAP 179

RESULT 10
US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-2

Query Match 58.8%; Score 211; DB 3; Length 361;
Best Local Similarity 55.7%; Pred. No. 1.5e-20;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGGQTSNDAAALNASSKEEALQIIRKIPKYLFPQHNLNSAL 60
Db 110 TIWGDQFIDGRSARGGQQTNDAYAKAINAGSKQALDVILREBQPKDFVLQNHINRSL 169

QY 61 AAFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 11
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match 58.8%; Score 211; DB 3; Length 361;
Best Local Similarity 55.7%; Pred. No. 1.5e-20;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGGQTSNDAAALNASSKEEALQIIRKIPKYLFPQHNLNSAL 60
Db 110 TIWGDQFIDGRSARGGQQTNDAYAKAINAGSKQALDVILREBQPKDFVLQNHINRSL 169
```



;  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mueller, Lisa V  
; REGISTRATION NUMBER: 38,978  
; REFERENCE/DOCKET NUMBER: SVS3801P0260  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-616-5400  
; TELEFAX: 312-616-5460  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 357 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-838-151A-24

Query Match 53.8%; Score 193; DB 3; Length 357;  
Best Local Similarity 62.3%; Pred. No. 4.3e-18;  
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 4 WGEFQVDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSALAAI 63  
Db 111 FGVSQIDGRSARGGQGSANDAYAEALNSGSKSEALNLKEKAPKDYILOFHNLSNLDRI 170  
QY 64 F 64  
Db 171 F 171

## RESULT 15

US-08-838-151A-27  
; Sequence 27, Application US/08838151A  
; Patent No. 6291743  
; GENERAL INFORMATION:  
; APPLICANT: Stout, John T  
; APPLICANT: Luu, Hang T  
; APPLICANT: Maxwell, Douglas  
; APPLICANT: Ahlquist, Paul  
; APPLICANT: Hanson, Steve  
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
; TITLE OF INVENTION: Genes  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
; STREET: Two Prudential Plaza, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838,151A  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mueller, Lisa V  
; REGISTRATION NUMBER: 38,978  
; REFERENCE/DOCKET NUMBER: SVS3801P0260  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-616-5400  
; TELEFAX: 312-616-5460  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 357 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-838-151A-27

Query Match 53.8%; Score 193; DB 3; Length 357;  
Best Local Similarity 62.3%; Pred. No. 4.3e-18;  
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;  
QY 4 WGEFQVDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSALAAI 63  
Db 111 FGVSQIDGRSARGGQGSANDAYAEALNSGSKSEALNLKEKAPKDYILOFHNLSNLDRI 170  
QY 64 F 64  
Db 171 F 171

Search completed: December 23, 2003, 08:59:35  
Job time : 12.6667 secs

GenCore version 5.1.6  
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QM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds  
(without alignments)

172.015 Million cell updates/sec

Title: US-09-289-346B-7

Perfect score: 359

Sequence: 1 TLVWGFQVDCGARGGCQT.....FOFHNLSALAAIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	ID	Description
1	359	100.0	70	10	US-09-289-346A-7	Sequence 7, Appli
2	342	95.3	70	10	US-09-289-346A-1	Sequence 1, Appli
3	342	95.3	356	10	US-09-289-346A-11	Sequence 11, Appli
4	334	93.0	70	10	US-09-289-346A-9	Sequence 9, Appli
5	331	92.2	70	10	US-09-289-346A-12	Sequence 12, Appli
6	330	91.9	70	10	US-09-289-346A-16	Sequence 16, Appli
7	328	91.4	70	10	US-09-289-346A-8	Sequence 8, Appli
8	328	91.4	70	10	US-09-289-346A-14	Sequence 14, Appli
9	327	91.1	70	10	US-09-289-346A-2	Sequence 2, Appli
10	327	91.1	70	10	US-09-289-346A-10	Sequence 10, Appli
11	326	90.8	70	10	US-09-289-346A-13	Sequence 13, Appli
12	324	90.3	70	10	US-09-289-346A-4	Sequence 4, Appli
13	324	90.3	70	10	US-09-289-346A-15	Sequence 15, Appli
14	321	89.4	70	10	US-09-289-346A-5	Sequence 5, Appli
15	318	88.6	70	10	US-09-289-346A-6	Sequence 6, Appli

16	310	86.4	70	10	US-09-289-346A-3	Sequence 3, Appli
17	68	18.9	447	9	US-09-989-722-369	Sequence 369, App
18	68	18.9	447	9	US-09-989-723-369	Sequence 369, App
19	68	18.9	447	9	US-09-989-279-369	Sequence 369, App
20	68	18.9	447	9	US-09-989-727-369	Sequence 369, App
21	68	18.9	447	10	US-09-989-731-369	Sequence 369, App
22	68	18.9	447	10	US-09-989-732-369	Sequence 369, App
23	68	18.9	447	10	US-09-991-073-369	Sequence 369, App
24	68	18.9	447	10	US-09-990-442-369	Sequence 369, App
25	68	18.9	447	10	US-09-991-163-369	Sequence 369, App
26	68	18.9	447	10	US-09-993-604-369	Sequence 369, App
27	68	18.9	447	10	US-09-990-456-369	Sequence 369, App
28	68	18.9	447	10	US-09-989-721-369	Sequence 369, App
29	68	18.9	447	10	US-09-992-598-369	Sequence 369, App
30	68	18.9	447	10	US-09-989-293A-369	Sequence 369, App
31	68	18.9	447	10	US-09-989-735-369	Sequence 369, App
32	68	18.9	447	10	US-09-990-444-369	Sequence 369, App
33	68	18.9	447	10	US-09-991-181-369	Sequence 369, App
34	68	18.9	447	10	US-09-989-730-369	Sequence 369, App
35	68	18.9	447	10	US-09-990-436-369	Sequence 369, App
36	68	18.9	447	10	US-09-993-687-369	Sequence 369, App
37	68	18.9	447	11	US-09-989-734-369	Sequence 369, App
38	68	18.9	447	11	US-09-997-653-369	Sequence 369, App
39	68	18.9	447	11	US-09-993-667-369	Sequence 369, App
40	68	18.9	447	11	US-09-997-428-369	Sequence 369, App
41	68	18.9	447	11	US-09-997-666-369	Sequence 369, App
42	68	18.9	447	11	US-09-990-438-369	Sequence 369, App
43	68	18.9	447	11	US-09-990-562-369	Sequence 369, App
44	68	18.9	447	11	US-09-990-711-369	Sequence 369, App
45	68	18.9	447	11	US-09-984-271-128	Sequence 128, App

ALIGNMENTS

RESULT 1

US-09-289-346A-7  
; Sequence 7, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Grullem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR FILING DATE: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (59)..(62)  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine  
; OTHER INFORMATION: replacements (NLDRI72->ALAA172).  
US-09-289-346A-7

Query Match	100.0%	Score 359;	DB 10;	Length 70;
Best Local Similarity	100.0%	Pred. No. 1.7e-33;		
Matches	70;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
QY	1	TLVWGFQVDCGARGGCQTNDAAAEALNASSKEALQIREKIPEKYLQFHNLSAL	60	
Db	1	TLVWGFQVDCGARGGCQTNDAAAEALNASSKEALQIREKIPEKYLQFHNLSAL	60	
QY	61	AAIFDKTPEP	70	

110 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 169

Db 110 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 169  
QY 61 AAIFDKTPEP 70  
Db 170 DRIFDKTPEP 179

## RESULT 4

US-09-289-346A-9  
; Sequence 9, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (10)  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine  
; OTHER INFORMATION: Replacement (D120->A120)

## US-09-289-346A-9

Query Match 93.0%; Score 334; DB 10; Length 70;  
Best Local Similarity 94.3%; Pred. No. 3.3e-36;  
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
Db 1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
QY 61 AAIFDKTPEP 70  
Db 61 DRIFDKTPEP 70

## RESULT 5

US-09-289-346A-12  
; Sequence 12, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (354)  
; OTHER INFORMATION: Unsure about sequence assignment

Query Match 92.2%; Score 331; DB 10; Length 70;

Db 61 AAIFDKTPEP 70

## RESULT 2

US-09-289-346A-1  
; Sequence 1, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (354)  
; OTHER INFORMATION: Unsure about sequence assignment

Query Match 95.3%; Score 342; DB 10; Length 70;  
Best Local Similarity 95.7%; Pred. No. 2.9e-37;  
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
Db 1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
QY 61 AAIFDKTPEP 70  
Db 61 DRIFDKTPEP 70

## RESULT 3

US-09-289-346A-11  
; Sequence 11, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 356  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (354)  
; OTHER INFORMATION: Unsure about sequence assignment

Query Match 95.3%; Score 342; DB 10; Length 356;  
Best Local Similarity 95.7%; Pred. No. 2.5e-36;  
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60





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; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
US-09-289-346A-2

Query Match          91.1%; Score 327; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 2.7e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLSAL 60
Db 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60

QY 61 AAIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAA136->LLL136).
US-09-289-346A-10

Query Match          91.1%; Score 327; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 2.7e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLSAL 60
Db 1 TLVWGEFQVDRSARGGCGTSDNLLLEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60

QY 61 AAIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
```

```
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-13

Query Match          90.8%; Score 326; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 3.7e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLSAL 60
Db 1 TLVWGEFQVDRSARGGCGTSDAAAAAEALNASSKEEALQIIREKIPEKYLQFPHNLSNL 60

QY 61 AAIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-4
; Sequence 4, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (42)..(44)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REK154->AAA154).
US-09-289-346A-4

Query Match          90.3%; Score 324; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 6.8e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFPHNLSAL 60
Db 1 TLVWGEFQVDRSARGGCGTSDNDAAEALNASSKEEALQIIRKIPKYLQFPHNLSNL 60

QY 61 AAIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
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; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match      90.3%; Score 324; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 6.8e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGCGCQTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
Db 1 TLVWGEFQVDRSARGCGCQTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

Qy 61 AAIFDKTPEP 70
Db 61 DRIFDKTPEP 70

RESULT 14
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (EKYI59->AAA159).
US-09-289-346A-5

Query Match      89.4%; Score 321; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 1.7e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGCGCQTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
Db 1 TLVWGEFQVDRSARGCGCQTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

Qy 61 AAIFDKTPEP 70
Db 61 DRIFDKTPEP 70
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RESULT 15
US-09-289-346A-6
; Sequence 6, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (52)..(55)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (QFHN165->AFAA165).
US-09-289-346A-6

Query Match      88.6%; Score 318; DB 10; Length 70;
Best Local Similarity 91.4%; Pred. No. 4.1e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDRSARGCGCQTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSAL 60
Db 1 TLVWGEFQVDRSARGCGCQTSDNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

Qy 61 AAIFDKTPEP 70
Db 61 DRIFDKTPEP 70

Search completed: December 23, 2003, 09:43:30
Job time : 76 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds  
(without alignments)  
673.181 Million cell updates/sec

Title: US-09-289-346B-7  
Perfect score: 359  
Sequence: 1 TLVWGFQVDSARGGCGQT.....FQHNLSALAAIFDKTPEP 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	342	95.3	352	1 QOCVLI	Al1 protein - toma
2	242	67.4	361	1 QOCVPT	Al1 protein - toma
3	229	63.8	358	2 S07594	hypothetical prote
4	222	61.8	362	1 JQ1887	Al1 protein - toma
5	216	60.2	349	2 JQ2300	replicase - pepp
6	216	60.2	349	2 S31875	Al1 protein - pepp
7	215	59.9	359	2 S39211	gene C1 protein -
8	212	59.1	385	2 S28360	Al1 protein - beet
9	211	58.8	359	2 S22593	hypothetical prote
10	210	58.5	355	1 QOCVLI	AVI protein - abut
11	207	57.7	358	1 JQ1870	Al1 protein - toma
12	205	57.1	351	2 JQ2327	Al1 protein - indi
13	205	57.1	359	2 S39235	gene C1 protein -
14	195	54.3	360	2 S59885	replication-associ
15	193	53.8	357	1 QOCVCI	Al1 protein - toma
16	120	33.4	131	2 S45059	AC1 protein (clone
17	107	29.8	347	1 QOCVSI	Al1 protein - squa
18	70	19.5	587	2 JCI419	Fc gamma (IgG) rec
19	68	18.9	447	2 T12544	hypothetical prote
20	64.5	18.0	491	2 A51836	leucine aminopepti
21	64	17.8	316	2 C92085	conserved hypothet
22	64	17.8	340	2 B97011	probably O-sialogl
23	63.5	17.7	1229	2 T48959	kinesin-like prote
24	63.5	17.7	1610	2 A46227	voltage-dependent
25	63.5	17.7	1646	2 JH0422	calcium channel al
26	63.5	17.7	2161	2 JH0564	calcium channel al
27	63.5	17.7	2181	2 A38198	voltage-dependent
28	63.5	17.7	2203	2 T42742	protein-Npi-phosph
29	62	17.3	154	2 AD3475	

30	62	17.3	245	2	S76632	hypothetical prote
31	62	17.3	714	2	C95382	probable ferrichro
32	61	17.0	1502	1	RGBYH1	CYC1/CYP3 transcri
33	60.5	16.9	276	2	AC2341	hypothetical prote
34	60.5	16.9	840	2	T36175	probable large ATP
35	59.5	16.6	208	2	E97702	hypothetical prote
36	59.5	16.6	224	2	I40474	pro-sigma-E proces
37	59.5	16.6	408	2	A99238	conserved hypothet
38	59.5	16.6	446	1	S17553	dyein beta heavy
39	59	16.4	338	2	AG3582	iron(III)-binding
40	59	16.4	345	2	AD3024	hypothetical prote
41	59	16.4	359	2	E98260	periplasmic bindin
42	59	16.4	370	2	T34050	hypothetical prote
43	59	16.4	384	1	W2ML41	E2 protein - human
44	59	16.4	2459	2	AF2136	peptide synthetase
45	58.5	16.3	136	2	T22240	hypothetical prote

## ALIGNMENTS

### RESULT 1

QOCVLI  
Al1 protein - tomato golden mosaic virus  
C:Species: tomato golden mosaic virus  
A:Note: host Nicotiana sp. (tobacco)  
C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Apr-1994  
C:Accession: A04170  
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.  
EMBO J. 3, 2197-2205, 1984  
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat  
A:Reference number: A04170  
A:Accession: A04170  
A:Molecule type: DNA  
A:Residues: 1-352 <HAM>  
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match	95.3%	Score 342;	DB 1;	Length 352;
Best Local Similarity	95.7%	Pred. No. 2.5e-31;		
Matches	67;	Conservative	0;	Mismatches 3;
		Indels	0;	Gaps 0;
QY	1	TLVWGFQVDSARGGCGQTSNDAAEAALNASSKEALQIIRKIPKYLQFHNLSAL	60	
DB	111	TLVWGFQVDSARGGCGQTSNDAAEAALNASSKEALQIIRKIPKYLQFHNLSNL	170	
QY	61	AAIFDKTPEP 70		
DB	171	DRIFDKTPEP 180		

### RESULT 2

QOCVPT  
Al1 protein - potato yellow mosaic virus (isolate Venezuela)  
C:Species: potato yellow mosaic virus  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jun-2000  
C:Accession: J00364  
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.  
J. Gen. Virol. 72, 1515-1520, 1991  
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel  
A:Reference number: J00362; MUID:91311403; PMID:1856690  
A:Accession: J00364  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-361 <COU>  
A:Cross-references: GB:D00940; NID:g222458; PIDN:BAA00782.1; PID:g222459  
C:Genetics:  
A:Map position: segment A  
C:Superfamily: tomato golden mosaic virus Al1 protein

# THE EFFECT OF COMMUNAL AND ECONOMIC FACTORS ON THE FORMATION OF A



JQ2327  
 A1: protein - Indian cassava mosaic virus  
 N: Alternate names: replication-associated protein  
 C: Species: Indian cassava mosaic virus  
 C: Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 20-Sep-1999  
 C: Accession: JQ2327; S35883  
 R: Hong, Y.G.; Robinson, D.J.; Harrison, B.D.  
 J. Gen. Virol. 74, 2437-2443, 1993  
 A: Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-transmitted geminiviruses from tomato  
 A: Reference number: JQ2326; MUID:94065670; PMID:8245859  
 A: Accession: JQ2327  
 A: Molecule type: DNA  
 A: Residues: 1-351 <NON>  
 A: Cross-references: EMBL:224758; NID:9395351; PIDN:CAA90891.1; PID:9584046  
 C: Superfamily: tomato golden mosaic virus A11 protein

Query Match 57.1%; Score 205; DB 2; Length 351;  
 Best Local Similarity 59.7%; Pred. No. 1.1e-15;  
 Matches 40; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 4 WGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSALAAI 63  
 DB 113 WGTFTQIDGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSALAAI 172

QY 64 FDKTPEP 70  
 DB 173 FTKPPPP 179

RESULT 13  
 S39235  
 gene C1 protein - tomato yellow leaf curl virus  
 C: Species: tomato yellow leaf curl virus  
 C: Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Sep-1997  
 C: Accession: S39235  
 R: Crespi, S.; Noris, E.; Vaira, A.; Bosco, D.; Accotto, G.  
 submitted to the EMBL Data Library, December 1993  
 A: Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.  
 A: Reference number: S39233  
 A: Accession: S39235  
 A: Status: preliminary  
 A: Molecule type: DNA  
 A: Residues: 1-359 <CRE>  
 A: Cross-references: EMBL:228390; NID:gl041671; PID:gl334964  
 C: Superfamily: tomato golden mosaic virus A11 protein

Query Match 57.1%; Score 205; DB 2; Length 359;  
 Best Local Similarity 55.1%; Pred. No. 1.1e-15;  
 Matches 38; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 2 LYWGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSALAAI 61  
 DB 111 LEWGTFTQIDGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSALAAI 170

QY 62 AFDKTPPEP 70  
 DB 171 KYFQVPPAP 179

RESULT 14  
 S59885  
 replication-associated protein C1 - tomato yellow leaf curl virus  
 C: Species: tomato yellow leaf curl virus  
 C: Date: 14-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 20-Sep-1999  
 C: Accession: S59885  
 R: Hong, Y.; Harrison, B.D.  
 submitted to the EMBL Data Library, February 1995  
 A: Description: Nucleotide sequences from tomato leaf curl viruses from different countries  
 A: Reference number: S58346  
 A: Accession: S59885  
 A: Status: preliminary  
 A: Molecule type: DNA

A: Residues: 1-360 <NON>  
 A: Cross-references: EMBL:248182; NID:9344838; PIDN:CAA88229.1; PID:9974211  
 C: Superfamily: tomato golden mosaic virus A11 protein

Query Match 54.3%; Score 195; DB 2; Length 360;  
 Best Local Similarity 57.6%; Pred. No. 1.6e-14;  
 Matches 38; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 4 WGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSALAAI 63  
 DB 113 FGVFQIDGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSALAAI 172

QY 64 FDKTPEP 69  
 DB 173 FTFSAE 178

RESULT 15  
 QQCVC1  
 A11 protein - tomato yellow leaf curl virus  
 N: Alternate names: C1 protein  
 C: Species: tomato yellow leaf curl virus  
 C: Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
 C: Accession: D40779  
 R: Navot, N.; Pichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.  
 Virology 185, 151-161, 1991  
 A: Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single  
 A: Reference number: A40779; MUID:92024070; PMID:1926771  
 A: Accession: D40779  
 A: Status: translation not shown  
 A: Molecule type: DNA  
 A: Residues: 1-357 <NAV>  
 A: Cross-references: GB:X15656; NID:962204; PIDN:CAA33688.1; PID:962207  
 C: Superfamily: tomato golden mosaic virus A11 protein

Query Match 53.8%; Score 193; DB 1; Length 357;  
 Best Local Similarity 52.3%; Pred. No. 2.7e-14;  
 Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 4 WGEFQVDSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSALAAI 63  
 DB 111 FGVFQIDGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPEKYLQFHNLSALAAI 170

QY 64 F 64  
 DB 171 F 171

Search completed: December 23, 2003, 09:05:23  
 Job time: 11 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds  
(without alignments)  
569.747 Million cell updates/sec

Title: US-09-289-346B-7

Perfect score: 359

Sequence: 1 TLVWGEFQVDSARGGCQT.....FQHNLSALAAIFDKTPEP 70

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	342	95.3	352	1 VAL1_TGMV	P03567 tomato gold
2	242	67.4	361	1 VAL1_PYMV	P27258 potato yell
3	229	63.8	358	1 VAL1_CLVK	P14982 cassava lat
4	229	63.8	358	1 VAL1_CLVN	P14972 cassava lat
5	222	61.8	362	1 VAL1_TYLC	P36279 tomato yell
6	216	60.2	349	1 VAL1_PHVU	Q06923 pepper huas
7	215	59.9	359	1 VAL1_TYLCU	P38609 tomato yell
8	212	59.1	358	1 VAL1_BCTV	P14991 beet curly
9	211	58.8	353	1 VAL1_BGMV	P05175 bean golden
10	211	58.8	359	1 VAL1_TYLCM	P27260 tomato yell
11	210	58.5	355	1 VAL1_ABMVW	P21947 abutilon no
12	207	57.7	361	1 VAL1_TMOV	Q06857 tomato mott
13	193	53.8	357	1 VAL1_TYLCV	P27259 tomato yell
14	107	29.8	347	1 VAL1_SLVCV	P29048 squash leaf
15	68	18.9	447	1 TBL2_HUMAN	Q9Y4P3 homo sapien
16	65.5	18.2	298	1 OLIG2_CHICK	Q90XB3 gallus gall
17	64.5	18.0	491	1 AMPA_ANASP	Q82064 anabaena sp
18	63.5	17.7	1610	1 CCAD_MESAU	Q99244 mesocricetu
19	63.5	17.7	2161	1 CCAD_HUMAN	Q01568 homo sapien
20	63.5	17.7	2203	1 CCAD_RAT	P27732 rattus norv
21	61.5	17.1	476	1 DGRE_HUMAN	Q96df8 homo sapien
22	61.5	17.1	479	1 DGRE_MOUSE	Q70279 mus musculu
23	61	17.0	1502	1 CYP1_YEAS	P12351 saccharomyc
24	59.5	16.6	224	1 SP2R_BACSU	P39151 bacillus su
25	59.5	16.6	4466	1 DYHC_TRIGR	P23098 tripeustes
26	59	16.4	370	1 CC37_CABEL	Q02108 caenorhabdi
27	59	16.4	387	1 VE2_HPV41	P27552 human papil
28	59	16.4	387	1 Y4PF_RHISN	P55615 rhizobium s
29	58.5	16.3	136	1 Y452_CABEL	Q62250 caenorhabdi
30	58.5	16.3	299	1 Y175_HELPJ	Q9ZMQ7 helicobacte
31	57.5	16.0	367	1 LHX4_MOUSE	P53776 mus musculu
32	57.5	16.0	1852	1 CCAS_CYPCA	P22316 cyprinus ca
33	57	15.9	247	1 YCP4_YEAS	P25349 saccharomyc

34 57 15.9 256 1 UT11\_YEAST  
35 56.5 15.7 511 1 HUTH\_VIBCH  
36 56.5 15.7 2190 1 CCAD\_CHICK  
37 56 15.6 98 1 VATF\_METJA  
38 56 15.6 295 1 VAL1\_CSMV  
39 56 15.6 295 1 VAL1\_TYDVA  
40 56 15.6 492 1 MOT3\_MOUSE  
41 56 15.6 492 1 MOT3\_RAT  
42 56 15.6 836 1 GCSR\_HUMAN  
43 55.5 15.5 266 1 ETFB\_MYCTU  
44 55.5 15.5 266 1 ETFB\_MYCTU  
45 55.5 15.5 428 1 GBA1\_CANAL

## ALIGNMENTS

RESULT 1  
VAL1\_TGMV STANDARD; PRT; 352 AA.

AC P03567; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE AL1 protein.

GN ACI.

OS Tomato golden mosaic virus (TGMV).

OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

OX NCBI\_TaxID=10831;

RN [1] SEQUENCE FROM N.A.

RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;

RT "Complete nucleotide sequence of the infectious cloned DNA components

of tomato golden mosaic virus: potential coding regions and regulatory

sequences.";

RL EMBO J. 3:2197-2205 (1984).

CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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CC EMBL; K02029; -; NOT ANNOTATED CDS.

DR PIR; A04170; QQCVL1.

DR InterPro; IPR001191; Gemini AL1.

DR Pfam; PF00799; Gemini AL1; 1.

DR PRINTS; PR00227; GEMCOATALL.

DR ProDom; PD000736; Gemini\_AL1; 1.

DR ATP-binding.

KW NP\_BIND 223 230 ATP (POTENTIAL).

SQ SEQUENCE 352 AA; 40332 MW; C33C938E9644B4A4 CRC64;

Query Match 95.3%; Score 342; DB 1; Length 352;

Best Local Similarity 95.7%; Pred. No. 4.9e-32;

Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGGCQTSNDAAAEALNASSKEALQIREKIPEKYLQFHNLSAL 60

DB 111 TLVWGEFQVDSARGGCQTSNDAAAEALNASSKEALQIREKIPEKYLQFHNLSNL 170

QY 61 AAIFDKTPEP 70

DB 171 DRIFDKTPEP 180

RESULT 2

VAL1\_PYMV

ID VAL1\_PYMV

STANDARD; PRT; 361 AA.

AC P27258;



```

01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
All protein.
Potato yellow mosaic virus (isolate Venezuela).
Viruses: ssDNA viruses, Geminiviridae, Begomovirus.
NCBI_TaxID=10828;
[1]
SEQUENCE FROM N.A.
MEDLINE=913111403; PubMed=1856690;
Coutts R.H.A.; Coffin R.S.; Roberts E.J.P., Hamilton W.D.O.;
"The nucleotide sequence of the infectious cloned DNA components of
potato yellow mosaic virus.";
J. Gen. Virol. 72:1515-1520(1991).
-/- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
-----
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EMBL; D00940; BRA00782.1; -.
PIR; JU0364; QOCVPT.
InterPro; IPR001191; Gemini_All.
Pfam; PF00799; Gemini_All; 1.
PRINTS; PR00227; GEMCOATAll.
ProDom; PD000736; Gemini_All; 1.
ATP-BIND.
NP_BIND 222 229 ATP (POTENTIAL).
SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;
Query Match 67.4%; Score 242; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 1.8e-20;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
QY 1 TLVWGFEQVQGRSARGGCGQTNDAAAEALNASKSEALQITREKIPEKLYFQFNLMSAL 60
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 110 TIWGLFQIDGRSARGGQTVNDAAAEALNSGTKAEAMKIKEKLPKFLFYHNLSCL 169
QY 61 AAIFDKTPE 69
||| ||| |||
Db 170 DRIFMKAPE 178
-----
RESULT 3
VAL1 CLVK STANDARD; PRT; 358 AA.
AC P14982.
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DT All1 protein (40.4 kDa protein).
DE AC1.
GN Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
-/- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
-----
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CC -----
DR EMBL: X70418; CAA49856.1; -.
DR FIR: JQ2300; JQ2300.
DR FIR: S31875; S31875.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATALL.
DR ProDom: PD000736; Gemini_AL1; 1.
DR ATP-binding.
DR NP_BIND 221 228 ATP (BY SIMILARITY).
DR NP_SEQUENCE 349 AA; 39722 MW; DSF4E76CDS6370F4 CRC64;
DR QUERY Match 60.2%; Score 216; DB 1; Length 349;
DR Best Local Similarity 59.6%; Pred. No. 1.7e-17;
DR Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
QY 1 TLVGEFQVDRSGAGCGQTSDAAALNASKEEALQIIREKIPEKYLFOFHNLSAL 60
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 TVWGEFQIDRSARGQQSQANDTYAKALNASAEALQIKEQPQHFLOFHNYSNA 169
QY 61 AAIFDKTPEP 70
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 170 NRIFQTPEP 179
RESULT 7
VAL1_TYLCU STANDARD; PRT; 359 AA.
ID VAL1_TYLCU
AC F38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 protein (Cl protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=37139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=942556836; PubMed=8198442;
RA Norris E., Hidalgo E., Accotto G., Morionese E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
RT from the west Mediterranean basin: the nucleotide sequence of an
RT infectious clone from Spain.";
RL Arch. Virol. 135:165-170(1994).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL: Z25751; CRA81026.1; -.
DR FIR: S39211; S39211.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATALL.
DR ProDom: PD000736; Gemini_AL1; 1.
DR ATP-binding.
DR NP_BIND 221 228 ATP (POTENTIAL).
DR NP_SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3EC CRC64;
DR QUERY Match 59.9%; Score 215; DB 1; Length 359;
DR Best Local Similarity 58.0%; Pred. No. 2.3e-17;
DR Matches 40; Conservative 9; Mismatches 20; Indels 0; Gaps 0;
QY 2 LVWGEFQVDRSGAGCGQTSDAAALNASKEEALQIIREKIPEKYLFOFHNLSALA 61
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 111 LEWGTFQIDGRSAGGQQTANDAYAKINAGSKSEALDVIKELAPRDYILHFNHNSNLD 170

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QY      62 AIFDKTPEP 70
Db      171 RVFQVPPAP 179

RESULT 8
VAL1_BCTV
ID VAL1_BCTV STANDARD; PRT; 358 AA.
AC P14931;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein (40.8 kDa protein).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
RT beet curly top virus."
RL EMBO J. 5:1761-1767(1986).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC
CC EMBL; M10070; AAA46318.1; .
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATAL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 58.8%; Score 211; DB 1; Length 353;
Best Local Similarity 58.6%; Pred. No. 5.1e-17;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY      1 TLVWGFQVDSARGGCGTSDNAAEALNASSKEEALQIREKIPKYLQFHNLSAL 60
Db      110 TIEWGFQVDSARGGCGTSDNAAEALNASSKEEALQIREKIPKYLQFHNLSAL 169
QY      61 AAIFDKTPEP 70
Db      170 QKIFQRPDP 179

RESULT 10
VAL1_TYLCM
ID VAL1_TYLCM STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AL1 protein (CI protein).
GN CI.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92107660; PubMed=1840676;
RA Khayat-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
RA Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a
RT whitely-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
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CC
CC EMBL; X61153; CAA43466.1; .
DR PIR; S22593; S22593.
DR PDB; 1L2M; 18-SEP-02.
DR PDB; 1L5I; 18-SEP-02.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1; 1.
DR PRINTS; PR00227; GEMCOATAL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding; 3D-structure.
FT NP BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 40733 MW; 9717BAA07C93EFA7 CRC64;

QY      62 AIFDKTPEP 70
Db      171 RVFQVPPAP 179

RESULT 9
VAL1_BGMV
ID VAL1_BGMV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE AL1 protein (40.2 kDa protein).
GN AC1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Howarth A.J., Caton J., Bossert M., Goodman R.M.;
RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
RT regulation in geminiviruses."
RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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Query Match      58.8%; Score 211; DB 1; Length 359;
Best Local Similarity 56.5%; Pred. No. 6.6e-17;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 LWGFEQVDRSGRGCGQTNDAAAEALNASSKEEALQIIREKIPKYLQFPHNLSALA 61
DB 111 LEWGTFTQDGRSARGGQQTANDAYAKAINAGSQALDVIKELAPRDYVLHFNHNSNLD 170
QY 62 AIFDKTPEP 70
DB 171 KVFQVPPAP 179

RESULT 11
VAL1 ABMYM
ID VAL1 ABMYM STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T.; Zimmatt G.; Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC EMBL; L14460; AAC32414.1; --
DR F1R; JQ1870; JQ1870.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 355 AA; 40257 MW; 16A2C8A63251E95 CRC64;

Query Match      58.5%; Score 210; DB 1; Length 355;
Best Local Similarity 57.1%; Pred. No. 8.5e-17;
Matches 40; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1 TLWGEFQVDRSGRGCGQTNDAAAEALNASSKEEALQIIREKIPKYLQFPHNLSAL 60
DB 110 TRWGEFQVDRSGRGCGQTNDAAAEALNASSKEEALQIIREKIPKYLQFPHNLSAL 169
QY 61 AIFDKTPEP 70
DB 170 ERIFAKAPEP 179

RESULT 12
VAL1 TMOV
ID VAL1 TMOV STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.

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GN AL1.
OS Tomato mottle virus (isolate Florida) (TMov).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9107858; PubMed=1469361;
RA Abouzid A.M.; Polson J.E.; Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
isolated from tomatoes in Florida.";
RL J. Gen. Virol. 73:3225-3229(1992).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC EMBL; L14460; AAC32414.1; --
DR F1R; JQ1870; JQ1870.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 8138B65CEEAC6950 CRC64;

Query Match      57.7%; Score 207; DB 1; Length 361;
Best Local Similarity 54.3%; Pred. No. 1.9e-16;
Matches 38; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLWGEFQVDRSGRGCGQTNDAAAEALNASSKEEALQIIREKIPKYLQFPHNLSAL 60
DB 110 TRWGEFQVDRSGRGCGQTNDAAAEALNASSKEEALQIIREKIPKYLQFPHNLSAL 169
QY 61 AIFDKTPEP 70
DB 170 ERIFAKAPEP 179

RESULT 13
VAL1 TYLCV
ID VAL1 TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9204070; PubMed=1926771;
RA Navot N.; Pichersky E.; Zeidan M.; Zamir D.; Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
with a single genomic component.";
RL Virology 185:151-161(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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DR EMBL; X15656; CAA33688.1; --
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 219 226 ATP (POTENTIAL).
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match
Best Local Similarity 53.8%; Score 193; DB 1; Length 357;
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 4 WGFQVDSRGSGGQTSNDAAEALNASSKEALQIIREKIPEKYLQFPHNLSALAAI 63
Db 111 FGVSDIGRSARGGQSQANDAAEALNASSKEALQIIREKIPEKYLQFPHNLSALDRI 170

Qy 64 F 64
Db 171 F 171

RESULT 14
VAL1 SLVC STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 01-DEC-1992 (Rel. 24, Last annotation update)
DE AL1 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G., Jazdzins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype.";
RL Virology 180:58-69(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; M38183; AAC32410.1; ALT_INIT.
DR PIR; C36785; QOCVSI.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDAEBDD122110E CRC64;

Query Match
Best Local Similarity 29.8%; Score 107; DB 1; Length 347;
Matches 23; Conservative 13; Mismatches 26; Indels 4; Gaps 1;

Qy 5 GEFQVDSRGSGGQTSNDAAEALNASSKEALQIIREKIPEKYLQFPHNLSALAAIF 64
Db 116 GQYKVSQ---GSKSNKDDVYHNAVNSAGSAGEALDIKAGDPKTFVYVNNLLANVERLP 171

Qy 65 DKTPEP 70
Db 172 QKPEP 177

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RESULT 15
TBL2_HUMAN STANDARD; PRT; 447 AA.
ID TBL2_HUMAN
AC Q9Y4P3; Q9Q0B2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transducin beta-like 2 protein (WS beta-transducin repeats protein).
DE (WS-betaTRP) (Williams-Beuren syndrome chromosome region 13 protein).
DE TBL2 OR WBSCTR13.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20044626; PubMed=10575226;
RA Perez Jurado L.A., Wang Y.-K., Francke U., Cruces J.;
RT "TBL2, a novel transducin family member in the WBS deletion:
RT characterization of the complete sequence, genomic structure,
RT transcriptional variants and the mouse ortholog.";
RL Cytogenet. Cell Genet. 86:277-284(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansoyge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
RN [3]
RP SEQUENCE OF 14-447 FROM N.A.
RX MEDLINE=99075645; PubMed=9860302;
RA Meng X., Lu X., Li Z., Green E.D., Massa H., Trask B.J., Morris C.A.,
RA Keating M.T.;
RT "Complete physical map of the common deletion region in Williams
RT syndrome and identification and characterization of three novel
RT genes.";
RL Hum. Genet. 103:590-599(1998).
CC -1- DISEASE: Haploinsufficiency of TBL2 may be the cause of certain
CC cardiovascular and musculo-skeletal abnormalities observed in
CC Williams-Beuren syndrome (WBS) [MIM:194050], a rare developmental
CC disorder. It is a contiguous gene deletion syndrome involving
CC genes from chromosome band 7q11.23.
CC -1- SIMILARITY: Contains 7 WD repeats.
CC -----
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CC -----
DR EMBL; AF097484; AAF06823.1; --
DR EMBL; AF097485; AAF06824.1; --
DR EMBL; AL080162; CAB45751.1; --
DR EMBL; AF056183; AAD28083.1; ALT_INIT.
DR PIR; T12544; T12544.
DR Genew; HGNC:11586; TBL2.
DR MIM; 605842; --
DR MIM; 194050; --
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 5.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 2.
DR SMART; SM00320; WD40; 5.

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DR PROSITE; PS00678; WD REPEATS_1; 1.
DR PROSITE; PS50082; WD REPEATS_2; 3.
DR PROSITE; PS50294; WD REPEATS_REGION; 1.
KW Repeat; WD repeat; Williams-Beuren syndrome.
FT REPEAT 88 127 WD 1.
FT REPEAT 134 174 WD 2.
FT REPEAT 186 226 WD 3.
FT REPEAT 228 267 WD 4.
FT REPEAT 277 316 WD 5.
FT REPEAT 329 367 WD 6.
FT REPEAT 371 409 WD 7.
SQ SEQUENCE 447 AA; 49797 MW; B260087E1A71D3F9 CRC64;

Query Match      18.9%; Score 68; DB 1; Length 447;
Best Local Similarity 32.7%; Pred. No. 2.7;
Matches 16; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

Qy 12 RSARGGQTSNDAAAEALNASSKEEALQIREKIPEKYLEQFHNLSAL 60
Db 38 RSGRPACQKANGPPDPKSGSKQKQYQIRKKEKPOHNFHRLAAAL 86

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Search completed: December 23, 2003, 08:57:40  
 Job time : 6.7778 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 25.3333 Seconds  
(without alignments)  
713.040 Million cell updates/sec

Title: US-09-289-346B-7

Perfect score: 359

Sequence: 1 TLVWGFQVDRSGCGCQT.....FOFHNLSALAAIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phage.\*

10: sp\_plant.\*

11: sp\_ricent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_virus.\*

16: sp\_bacteriaph.\*

17: sp\_archaeap.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	293	81.6	351	Q91R10	Q91R10 tomato seve
2	291	81.1	352	Q9E000	Q9E000 tomato rugo
3	283	78.8	232	Q8QPV3	Q8QPV3 tomato chlo
4	274	76.3	226	Q9WHF6	Q9WHF6 tomato mild
5	274	76.3	226	Q09727	Q09727 leonurus mo
6	272	75.8	361	Q67574	Q67574 bean golden
7	270	75.2	225	Q9QDB1	Q9QDB1 cowpea gold
8	270	75.2	314	Q9ELT8	Q9ELT8 sweet potat
9	270	75.2	364	Q9QS55	Q9QS55 sweet potat
10	267	74.4	185	Q98693	Q98693 sida golden
11	263	73.3	235	Q8QPU4	Q8QPU4 tomato infe
12	262	73.0	208	Q8TLV3	Q8TLV3 potato yell
13	262	73.0	289	Q8JLY5	Q8JLY5 potato yell
14	259	72.1	149	Q88975	Q88975 macroptiliu
15	259	72.1	233	Q9YLA4	Q9YLA4 macroptiliu
16	258	71.9	234	Q39180	Q39180 geminivirid

17	258	71.9	361	12	Q8JMW4	Q8JMW4 potato yell
18	256	71.3	360	12	Q8QMH4	Q8QMH4 sida mottle
19	254	70.8	361	12	Q8QVH0	Q8QVH0 ageratum en
20	252	70.2	190	12	Q9Z089	Q9Z089 tobacco lea
21	252	70.2	190	12	Q9Z084	Q9Z084 tobacco lea
22	251	69.9	223	12	Q8QPU7	Q8QPU7 tomato seve
23	249	69.4	190	12	Q9W827	Q9W827 tobacco lea
24	249	69.4	208	12	Q9Z0C4	Q9Z0C4 tobacco lea
25	249	69.4	353	12	Q72692	Q72692 beet curly
26	249	69.4	354	12	Q65438	Q65438 beet curly
27	249	69.4	359	12	Q91M88	Q91M88 tobacco lea
28	249	69.4	359	12	Q8JVE8	Q8JVE8 tomato curl
29	247	68.8	208	12	Q9Z0C0	Q9Z0C0 tobacco lea
30	247	68.8	208	12	Q9Z0B8	Q9Z0B8 tobacco lea
31	246	68.5	203	12	Q9Z0B6	Q9Z0B6 tobacco lea
32	245	68.2	208	12	Q9Z0B6	Q9Z0B6 tobacco lea
33	245	68.2	358	12	Q65418	Q65418 beet curly
34	244	68.0	363	12	Q73577	Q73577 cotton leaf
35	239	66.6	359	12	Q91B86	Q91B86 ageratum ye
36	239	66.6	360	12	Q9DX10	Q9DX10 ageratum ye
37	238	66.3	190	12	Q9Z086	Q9Z086 tobacco lea
38	238	66.3	248	12	Q911W5	Q911W5 macroptiliu
39	238	66.3	362	12	Q56816	Q56816 chayote mos
40	237	66.0	208	12	Q9Z0A0	Q9Z0A0 tobacco lea
41	237	66.0	362	12	Q8V016	Q8V016 cotton leaf
42	237	66.0	362	12	Q8V018	Q8V018 cotton leaf
43	237	66.0	362	12	Q8V618	Q8V618 cotton leaf
44	237	66.0	362	12	Q8V0H6	Q8V0H6 okra leaf c
45	237	66.0	362	12	Q9IN48	Q9IN48 okra enatio

ALIGNMENTS

RESULT 1

Q91R10 ID Q91R10 PRELIMINARY; PRT; 351 AA.  
AC Q91R10; 01-DEC-2001 (TEMBLrel. 19, Created)  
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
DE Rep protein.  
GN ACI.  
OS Tomato severe rugose virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_taxid=158463;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Minas Gerais;  
RA Rezende W.L., Goulart L.R., Parreira K.S., Figueiredo J.E.F.;  
RT "The full-length DNA-A nucleotide sequence of a novel tomato-infecting begomovirus, Tomato severe rugose virus, in Brazil."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY029750; AAK50357.1;  
DR InterPro; IPR001191; Gemini\_A1.  
DR Pfam; PF00799; Gemini\_A1; 1.  
DR PRINTS; PR00227; GEMCOATL1.  
DR ProDom; PD000736; Gemini\_A1; 1.  
SQ SEQUENCE 351 AA; 40122 MW; 87F937A4F873B6CF CRC64;

Query Match 81.6%; Score 293; DB 12; Length 351;

Best Local Similarity 78.8%; Pred. No. 5.1e-26;

Matches 55; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 TLVWGFQVDRSGCGCQTSDAAALNASKEALQIIEKIPEKYLQFHNLSAL 60

Db 111 TIENGEFOIDGRSGCGCQTANDAAALNASKDVALQIIEKLPKFLQFHNLSNL 170

QY 61 AAFDKTPEP 70

Db 171 DRIFARAPEP 180

110 TLEWGEFQIDGRSARGGQQTNDAAALNASSKEAMQIIEKLPKFLFOYHNLSSL 169

110 TLEWGEFQIDGRSARGGQQTNDAAALNASSKEAMQIIEKLPKFLFOYHNLSSL 169

Db QY 61 AAFDKTPEP 70  
170 DRIFSKAPEP 179

RESULT 4  
Q9WHF6 PRELIMINARY; PRT; 226 AA.  
ID Q9WHF6  
AC Q9WHF6  
DT 01-NOV-1999 (TREMELrel. 12, Created)  
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)  
DE Replication-associated protein (fragment).  
GN REP.  
OS Tomato mild mottle geminivirus.  
OC Viruses; ssDNA viruses; Geminiviridae; unclassified Geminiviridae.  
OX NCBI\_TaxID=92943;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HN96-H5Kw;  
RA Nakhla M.K., Mejia L., Ramirez P., Karkashian J.P., Doyle M.M., Maxwell D.P.;  
RT "Molecular characterization and DNA-based detection methods for vegetable-infecting geminiviruses in Central America."  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF131071; AAD33471.1;  
DR InterPro; IPR001191; Geminini\_AL1.  
DR Pfam; PF00799; Geminini\_AL1.  
DR PRINTS; PR00227; GEMCOATALL.  
DR ProDom; PD000736; Geminini\_AL1; 1.  
FT NON\_TER 226 226  
SQ SEQUENCE 226 AA; 25941 MW; 2EA4116712871A23 CRC64;

Query Match 76.3%; Score 274; DB 12; Length 226;  
Best Local Similarity 72.9%; Pred. No. 5.1e-24;  
Matches 51; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLVWGEFQIDGRSARGGQQTNDAAALNASSKEAMQIIEKLPKFLFOYHNLSSL 60  
111 TLVWGEFQIDGRSARGGQQTNDAAALNASSKEAMQIIEKLPKFLFOYHNLSSL 170

Db QY 61 AAFDKTPEP 70  
171 DRIFSKAPEP 180

RESULT 5  
Q09727 PRELIMINARY; PRT; 226 AA.  
ID Q09727  
AC Q09727  
DT 01-JUL-1997 (TREMELrel. 04, Created)  
DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
DE Rep protein (fragment).  
GN REP.  
OS Leucurus mosaic virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=58177;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LeMV- Brazil 1;  
RA Faria J.C., Maxwell D.P.;  
RT "Variability in geminivirus associated with Phaseolus vulgaris in Brazil."  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U92532; AAB51157.1;  
DR InterPro; IPR001191; Geminini\_AL1.  
DR Pfam; PF00799; Geminini\_AL1.  
DR PRINTS; PR00227; GEMCOATALL.  
DR ProDom; PD000736; Geminini\_AL1; 1.  
FT NON\_TER 226 226

Db QY 61 AAFDKTPEP 70  
171 DRIFSKAPEP 180

RESULT 3  
Q8QPV3 PRELIMINARY; PRT; 232 AA.  
ID Q8QPV3  
AC Q8QPV3  
DT 01-JUN-2002 (TREMELrel. 21, Created)  
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)  
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
DE Replication-associated protein (fragment).  
GN AC1.  
OS Tomato chlorotic vein virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=172390;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DF-Bri;  
RA Ribeiro S.G., Ambrozovic L.P., de Avila A.C., Calegario R.F., Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;  
RT "Distribution and genetic diversity of tomato-infecting geminiviruses in Brazil."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY049205; AAL82824.1;  
DR InterPro; IPR001191; Geminini\_AL1.  
DR Pfam; PF00799; Geminini\_AL1;  
DR ProDom; PD000736; Geminini\_AL1; 1.  
FT NON\_TER 232 232  
SQ SEQUENCE 232 AA; 26319 MW; 254CA5D040D35DDA CRC64;

Query Match 78.8%; Score 283; DB 12; Length 232;  
Best Local Similarity 77.1%; Pred. No. 4.7e-25;  
Matches 54; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQIDGRSARGGQQTNDAAALNASSKEAMQIIEKLPKFLFOYHNLSSL 60  
111 TLVWGEFQIDGRSARGGQQTNDAAALNASSKEAMQIIEKLPKFLFOYHNLSSL 170

Db QY 61 AAFDKTPEP 70  
171 DRIFSKAPEP 180

RESULT 3  
Q8QPV3 PRELIMINARY; PRT; 232 AA.  
ID Q8QPV3  
AC Q8QPV3  
DT 01-JUN-2002 (TREMELrel. 21, Created)  
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)  
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
DE Replication-associated protein (fragment).  
GN AC1.  
OS Tomato chlorotic vein virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=172390;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DF-Bri;  
RA Ribeiro S.G., Ambrozovic L.P., de Avila A.C., Calegario R.F., Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;  
RT "Distribution and genetic diversity of tomato-infecting geminiviruses in Brazil."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY049205; AAL82824.1;  
DR InterPro; IPR001191; Geminini\_AL1.  
DR Pfam; PF00799; Geminini\_AL1;  
DR ProDom; PD000736; Geminini\_AL1; 1.  
FT NON\_TER 232 232  
SQ SEQUENCE 232 AA; 26319 MW; 254CA5D040D35DDA CRC64;

Query Match 78.8%; Score 283; DB 12; Length 232;  
Best Local Similarity 77.1%; Pred. No. 4.7e-25;  
Matches 54; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQIDGRSARGGQQTNDAAALNASSKEAMQIIEKLPKFLFOYHNLSSL 60  
111 TLVWGEFQIDGRSARGGQQTNDAAALNASSKEAMQIIEKLPKFLFOYHNLSSL 170



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SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E76083FC5 CRC64;
Query Match 76.3%; Score 274; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 5.1e-24;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSGRGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSAL 60
Db 111 TVWGFQVDRSGRGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 170

Qy 61 AAIFDKTPEP 70
Db 171 DRIFAKAPEP 180

RESULT 6
Q67574 PRELIMINARY; PRT; 361 AA.
AC Q67574;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative replicative protein.
GN ALI.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RA "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration."
RL Phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RT "Differentiation of bean-infecting geminiviruses by nucleic acid
RT hybridization probes and aspects of bean golden mosaic in Brazil."
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus."
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M88686; AAA46312.1; -.
DR InterPro; IPR001191; Gemin_iAL1.
DR Pfam; PF00799; Gemin_iAL1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemin_iAL1.
DR ProDom; PD000736; Gemin_iAL1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 75.8%; Score 272; DB 12; Length 361;
Best Local Similarity 76.1%; Pred. No. 1.5e-23;
Matches 51; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 4 WGFQVDRSGRGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSALAI 63
Db 113 WGFQVDRSGRGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNLDRI 172

Qy 64 FDKTPEP 70
Db 173 FTKAPDP 179

RESULT 7
Q9QDB1 PRELIMINARY; PRT; 225 AA.
ID Q9QDB1
AC Q9QDB1;

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DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Cowpea golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CGMV-BR;
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RT Brazil."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF188708; AAF06318.1; -.
DR InterPro; IPR001191; Gemin_iAL1.
DR Pfam; PF00799; Gemin_iAL1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemin_iAL1.
DR ProDom; PD000736; Gemin_iAL1.
FT NON TER 225
SQ SEQUENCE 225 AA; 25766 MW; 1089CB6BD15B5D CRC64;

Query Match 75.2%; Score 270; DB 12; Length 225;
Best Local Similarity 76.1%; Pred. No. 1.5e-23;
Matches 51; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 4 WGFQVDRSGRGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSALAI 63
Db 113 WGFQVDRSGRGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNLDRI 172

Qy 64 FDKTPEP 70
Db 173 FKKPPPP 179

RESULT 8
Q9ELT8 PRELIMINARY; PRT; 314 AA.
ID Q9ELT8
AC Q9ELT8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Replication associated protein.
GN ACI.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States."
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288227; AAG01006.1; -.
DR InterPro; IPR001191; Gemin_iAL1.
DR Pfam; PF00799; Gemin_iAL1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemin_iAL1.
DR ProDom; PD000736; Gemin_iAL1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 75.2%; Score 270; DB 12; Length 314;
Best Local Similarity 79.4%; Pred. No. 2.2e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 TLVWGFQVDRSGRGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSAL 60
Db 110 TLVWGFQVDRSGRGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 169

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QY 61 AAIFDKTP 68
DB 170 DRIFSPPP 177

RESULT 9
Q9QS55 PRELIMINARY; PRT; 364 AA.
AC Q9QS55;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl virus; nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-line 0:0-0(1999).
DR EMBL; AF104036; AAD47173.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Geminini_AL1.1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 75.2%; Score 270; DB 12; Length 364;
Best Local Similarity 79.4%; Pred. No. 2.7e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSRGSGCQTNDAAAEALNASSKEEALQIIREKIPKYLFOFHNLSAL 60
DB 110 TITWGFQVDSRGSGCQTNDAAAEALNASSKEEALQIIREKIPKYLFOFHNLSNL 169
QY 61 AAIFDKTP 68
DB 170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica;
RC Roye M.B., McLaughlin W.A., Nakha N.K., Maxwell D.P.;
RT "Genetic Diversity among Geminiviruses associated with the weed species Sida spp, Macroptilium lathyroides, and Wissadula ampliissima from Jamaica.";
RL Plant Dis. 81:1251-1258(1997).
DR EMBL; U67926; AAB97865.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.

QY 61 AAIFDKTP 68
DB 170 DRIFSPPP 177

RESULT 11
Q8QPU4 PRELIMINARY; PRT; 235 AA.
AC Q8QPU4;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RA Ribeiro S.G., Ambrozovic L.P., de Avila A.C., Calegario R.P.,
RT "Distribution and genetic diversity of tomato-infecting geminiviruses in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049208; AAL82833.1; -.
DR InterPro; IPR001191; Geminini_AL1.
DR Pfam; PF00799; Geminini_AL1.1.
DR ProDom; PD000736; Geminini_AL1.1.
FT NON TER 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BE0DD9C810 CRC64;

Query Match 73.3%; Score 263; DB 12; Length 235;
Best Local Similarity 73.1%; Pred. No. 1e-22;
Matches 49; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 4 WGEFQVDSRGSGCQTNDAAAEALNASSKEEALQIIREKIPKYLFOFHNLSALA 63
DB 113 WGFQVDSRGSGCQTNDAAAEALNASSKEEALQIIREKIPKYLFOFHNLSNLDRI 172
QY 64 FDKTPEP 70
DB 173 FTKAPDP 179

RESULT 12
Q8JULY3 PRELIMINARY; PRT; 208 AA.
AC Q8JULY3;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

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RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126611; AAM95993.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1.1.
FT NON TER 208
SQ SEQUENCE 208 AA; 23667 MW; 51211D59FAD690A6 CRC64;

Query Match 73.0%; Score 262; DB 12; Length 208;
Best Local Similarity 70.0%; Pred. No. 1.2e-22;
Matches 49; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGQTSNDAAAEALNASSKEALQIIRKIPKYLQFQHNLSAL 60
Db 110 TLVWGEFQVDRSGRGCGQTSNDAAAEALNASSKEALQIIRKIPKYLQFQHNLSAL 169

QY 61 AAIFDKTPEP 70
Db 170 DRIFMKADKP 179

RESULT 13
QBULY5 PRELIMINARY; PRT; 289 AA.
AC Q8JLY5;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;
RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY126610; AAM95993.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1.1.
FT NON TER 289
SQ SEQUENCE 289 AA; 32971 MW; 4ECF52F4C69C6764 CRC64;

Query Match 73.0%; Score 262; DB 12; Length 289;
Best Local Similarity 70.0%; Pred. No. 1.8e-22;
Matches 49; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGQTSNDAAAEALNASSKEALQIIRKIPKYLQFQHNLSAL 60
Db 110 TLVWGEFQVDRSGRGCGQTSNDAAAEALNASSKEALQIIRKIPKYLQFQHNLSAL 169

QY 61 AAIFDKTPEP 70
Db 170 DRIFMKADKP 179

RESULT 14
P88975 PRELIMINARY; PRT; 149 AA.
AC P88975;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;

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RN SEQUENCE FROM N.A.
RP STRAIN=Jamaican;
RA Roye M.E.;
RL Thesis (1996), Biochemistry, University of the West Indies, Jamaica.
DR EMBL; U75278; AAB36919.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1.1.
FT NON TER 149
SQ SEQUENCE 149 AA; 16785 MW; E4CF5BED4C9CD508 CRC64;

Query Match 72.1%; Score 259; DB 12; Length 149;
Best Local Similarity 68.6%; Pred. No. 1.8e-22;
Matches 48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGQTSNDAAAEALNASSKEALQIIRKIPKYLQFQHNLSAL 60
Db 52 TLVWGEFQVDRSGRGCGQTSNDAAAEALNASSKEALQIIRKIPKYLQFQHNLSAL 111

QY 61 AAIFDKTPEP 70
Db 112 DRIFMKADKP 121

RESULT 15
Q9YLA4 PRELIMINARY; PRT; 233 AA.
ID Q9YLA4;
AC Q9YLA4;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica strain 1;
RA Roye M.E.;
RT "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Jamaica strain 1;
RA Roye M.E., McLaughlin W.A., Maxwell D.P.;
RT "Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098940; RAD17850.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1.1.
FT NON TER 233
SQ SEQUENCE 233 AA; 26356 MW; AA490AF4D2166A02 CRC64;

Query Match 72.1%; Score 259; DB 12; Length 233;
Best Local Similarity 68.6%; Pred. No. 3e-22;
Matches 48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDRSGRGCGQTSNDAAAEALNASSKEALQIIRKIPKYLQFQHNLSAL 60
Db 110 TLVWGEFQVDRSGRGCGQTSNDAAAEALNASSKEALQIIRKIPKYLQFQHNLSAL 169

QY 61 AAIFDKTPEP 70
Db 170 DRIFMKADKP 179

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Search completed: December 23, 2003, 09:03:36  
Job time : 25.3333 secs

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# OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds  
(without alignments)  
340.128 Million cell updates/sec

Title: US-09-289-346B-8  
Perfect score: 361  
Sequence: 1 TLVNGEAAVDGRSARGGQT.....PQFHNLNSLDRIDFKTPEP 70

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361	100.0	70	21 AAB18684	Mutant peptide der
2	350	97.0	70	21 AAB18677	Peptide fragment f
3	350	97.0	356	21 AAB18687	Amino acid sequenc
4	342	94.7	70	21 AAB18685	Mutant peptide der
5	339	93.9	70	21 AAB18688	Mutant peptide der
6	338	93.6	70	21 AAB18692	Mutant peptide der
7	336	93.1	70	21 AAB18690	Mutant peptide der
8	335	92.8	70	21 AAB18678	Mutant peptide der
9	335	92.8	70	21 AAB18686	Mutant peptide der

10	334	92.5	70	21 AAB18689	Mutant peptide der
11	332	92.0	70	21 AAB18680	Mutant peptide der
12	332	92.0	70	21 AAB18691	Mutant peptide der
13	329	91.1	70	21 AAB18681	Mutant peptide der
14	328	90.9	70	21 AAB18683	Mutant peptide der
15	326	90.3	70	21 AAB18682	Mutant peptide der
16	318	88.1	70	21 AAB18679	Mutant peptide der
17	223.5	61.9	50	23 AAO22043	Retinoblastoma-bin
18	216	59.8	353	18 AAW34338	Bean golden mosaic
19	216	59.8	353	18 AAW34332	Bean golden mosaic
20	216	59.8	353	18 AAW34333	Bean golden mosaic
21	216	59.8	353	18 AAW34334	Bean golden mosaic
22	216	59.8	353	18 AAW34335	Bean golden mosaic
23	216	59.8	359	17 AAR88870	Sardinian tomato y
24	216	59.8	359	17 AAR88871	Sardinian tomato y
25	216	59.8	359	17 AAR88872	Sardinian tomato y
26	214	59.3	353	8 AAP70407	ORF 4 gene product
27	214	59.3	361	18 AAW34336	Tomato mottle viru
28	214	59.3	361	18 AAW34324	Tomato mottle viru
29	214	59.3	361	18 AAW34325	Tomato mottle viru
30	214	59.3	361	18 AAW34326	Tomato mottle viru
31	212	58.7	357	18 AAW34329	Tomato yellow leaf
32	212	58.7	357	18 AAW34330	Tomato yellow leaf
33	212	58.7	357	18 AAW34331	Tomato yellow leaf
34	207.5	57.5	361	8 AAP70562	Product of ORF 4 f
35	204	56.5	357	18 AAW34337	Tomato yellow leaf
36	202	56.0	362	19 AAW56495	Tobacco leaf curl
37	101	28.0	142	24 ABP58120	Tomato yellow leaf
38	71.5	19.8	945	22 ABB65231	Drosophila melanog
39	68.5	19.0	1693	21 ABA48457	Human laminin 5 po
40	68.5	19.0	1693	21 ABA48459	Human laminin 5 po
41	68.5	19.0	1713	16 AAR70148	Deduced sequence o
42	68.5	19.0	1713	21 ABA48458	Human laminin 5 po
43	68.5	19.0	1724	21 ABA48456	Human laminin 5 po
44	66.5	18.4	512	19 AAW68473	HIV-1 strain YBF30
45	66.5	18.4	665	22 ABB70991	Drosophila melanog

## ALIGNMENTS

### RESULT 1

AAB18684  
ID AAB18684 standard; peptide; 70 AA.

XX AAB18684;  
AC

XX 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
KW ribosome binding region; resistance; geminivirus infection.

OS Synthetic.

OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 7 /note= "wild type residue replaced with Ala"

FT Misc-difference 8 /note= "wild type residue replaced with Ala"

XX WO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UUNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Claim 52; Page 45; 73pp; English.  
 XX The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX SQ Sequence 70 AA;  
 Query Match 100.0%; Score 361; DB 21; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-38;  
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TLVWGEAAVDGRSARGCGCQTSDAAAEALNASSKEEALQIIREKIPKYLQFQHNLSNL 60  
 Db 1 TLVWGEAAVDGRSARGCGCQTSDAAAEALNASSKEEALQIIREKIPKYLQFQHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 Db 61 DRIFDKTPEP 70  
 RESULT 2  
 AAB18677  
 ID AAB18677 standard; peptide; 70 AA.  
 XX AAB18677;  
 AC AAB18677;  
 XX 22-JAN-2001 (first entry)  
 DE Peptide fragment from Rep protein of TGMV (amino acids 110-179).  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX Tomato golden mosaic virus.  
 OS WO200054573-Al.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX (UUNC-) UNIV NORTH CAROLINA STATE.  
 PA Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT -  
 XX Disclosure; Page 18; 73pp; English.  
 XX The present sequence is derived from a geminivirus replication (Rep)  
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,  
 CC catalyzes cleavage and ligation of single-stranded DNA, and interacts  
 CC with other viral and host proteins. Mutants of the AL1 protein are used  
 CC to produce transgenic plants. The mutation in AL1 is present in a  
 CC ribosome binding region, and expression of mutant AL1 protein imparts  
 CC increased resistance to geminivirus infection in the plant. Mutant AL1  
 CC proteins are useful for producing plants having increased resistance or  
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,  
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl  
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato  
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,  
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or  
 CC beet curly top virus.  
 XX SQ Sequence 70 AA;  
 Query Match 97.0%; Score 350; DB 21; Length 70;  
 Best Local Similarity 97.1%; Pred. No. 2.1e-36;  
 Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TLVWGEAAVDGRSARGCGCQTSDAAAEALNASSKEEALQIIREKIPKYLQFQHNLSNL 60  
 Db 1 TLVWGEAAVDGRSARGCGCQTSDAAAEALNASSKEEALQIIREKIPKYLQFQHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 Db 61 DRIFDKTPEP 70  
 RESULT 3  
 AAB18687  
 ID AAB18687 standard; peptide; 356 AA.  
 XX AAB18687;  
 AC AAB18687;  
 XX 22-JAN-2001 (first entry)  
 DE Amino acid sequence of a geminivirus replication protein of TGMV.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX Tomato golden mosaic virus.  
 OS WO200054573-Al.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX (UUNC-) UNIV NORTH CAROLINA STATE.  
 PA Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region

PT	-
XX	Disclosure; Page 47-48; 73pp; English.
XX	
XX	The present sequence represents a geminivirus replication (Rep) protein, which is also known as AL1. AL1 binds double-stranded DNA, catalyses cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the AL1 protein are used to produce transgenic plants. The mutation in AL1 is present in a ribosome binding region, and expression of mutant AL1 protein imparts increased resistance to geminivirus infection in the plant. Mutant AL1 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.
XX	
XX	Sequence 356 AA;
XX	
XX	Query Match 97.0%; Score 350; DB 21; Length 356;
XX	Best Local Similarity 97.1%; Pred. No. 1.7e-35;
XX	Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX	
Qy	1 TLVWGGAADVGRSARGGQTSNDAAAEALNASSKEEALQITREKIPKYLQFHNLSNL 60
Db	110 TLVWGEFQVDGRSARGGQTSNDAAAEALNASSKEEALQITREKIPKYLQFHNLSNL 169
Qy	61 DRIFDKTPEP 70
Db	170 DRIFDKTPEP 179
XX	
XX	RESULT 4
XX	AAB18685
ID	ABE18685 standard; peptide; 70 AA.
XX	AAB18685;
AC	
XX	
DT	22-JAN-2001 (first entry)
XX	
DE	Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX	
XX	Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW	ribosome binding region; resistance; geminivirus infection.
XX	
OS	Synthetic.
OS	Tomato golden mosaic virus.
XX	
PH	Key Location/Qualifiers
FT	Misc-difference 10
FT	/note= "wild type residue replaced with Ala"
XX	
PN	W0200054573-Al.
XX	
PD	21-SEP-2000.
XX	
XX	15-MAR-2000; 2000WO-US06759.
XX	
PR	18-MAR-1999; 99US-0125004.
PR	09-APR-1999; 99US-0289346.
XX	
XX	(UYNC-) UNIV NORTH CAROLINA STATE.
XX	
PI	Hanley-Bowdoin L, Orozco BM, Kong L;
XX	
DR	WPI; 2000-618851/59.
XX	
PT	Transgenic plants with increased resistance to geminivirus infection
PT	comprise a nucleic acid construct containing a nucleic acid sequence
PT	encoding a mutant AL1 protein with a mutation in the Rb binding region
PT	-

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PT - encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
PS Disclosure; Page 48; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 93.9%; Score 339; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 5.2e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 TLVWGEAAVDGRSARGGCGTSDNDAALNASSKEEALQIIREKIPKYLQFHNLSNL 60
Db 1 TLVWGEFQVDRSARGGCAASNDAAALNASSKEEALQIIREKIPKYLQFHNLSNL 60
Qy 61 DRIPDKTPEP 70
Db 61 DRIPDKTPEP 70
RESULT 6
AAB18692
ID AAB18692 standard; peptide; 70 AA.
AC AAB18692;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 66 /note= "wild type residue replaced with Ala"
FT Misc-difference 69 /note= "wild type residue replaced with Ala"
FT
XX WO200054573-Al.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
PT

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```

PT - encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
PS Disclosure; Page 50; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 93.6%; Score 338; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 6.9e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 TLVWGEAAVDGRSARGGCGTSDNDAALNASSKEEALQIIREKIPKYLQFHNLSNL 60
Db 1 TLVWGEFQVDRSARGGCGTSDNDAALNASSKEEALQIIREKIPKYLQFHNLSNL 60
Qy 61 DRIPDKTPEP 70
Db 61 DRIPDKTPEP 70
RESULT 7
AAB18690
ID AAB18690 standard; peptide; 70 AA.
AC AAB18690;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 27 /note= "wild type residue replaced with Ala"
FT Misc-difference 30 /note= "wild type residue replaced with Ala"
FT
XX WO200054573-Al.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
PT

```



PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX  
 XX  
 XX  
 XX Disclosure; Page 49; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 XX Sequence 70 AA;  
 SQ  
 Query Match 93.1%; Score 336; DB 21; Length 70;  
 Best Local Similarity 94.3%; Pred. No. 1.2e-34;  
 Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TLVWGEAAVDGRSARGGCGTSDNDAALNASSKEALQIREKIPEKYLQFPHNLSNL 60  
 DB 1 TLVWGEFQVDRSARGGCGTSDNDAALNASSKEALQIREKIPEKYLQFPHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 8  
 AAB18678  
 ID AAB18678 standard; peptide; 70 AA.  
 AC AAB18678;  
 XX  
 XX 22-JAN-2001 (first entry)  
 XX  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 XX Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 12 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 13 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 15 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 15 /note= "wild type residue replaced with Ala"  
 XX  
 XX WO200054573-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 XX 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX Hanley-Bowdoin L, Orozco BM, Kong L;  
 XX

DR WPI; 2000-618851/59.  
 XX  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT  
 PT  
 XX  
 XX Claim 53; Page 42-43; 73pp; English.  
 XX  
 CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.  
 XX  
 XX Sequence 70 AA;  
 SQ  
 Query Match 92.8%; Score 335; DB 21; Length 70;  
 Best Local Similarity 92.9%; Pred. No. 1.7e-34;  
 Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TLVWGEAAVDGRSARGGCGTSDNDAALNASSKEALQIREKIPEKYLQFPHNLSNL 60  
 DB 1 TLVWGEFQVDRSARGGCGTSDNDAALNASSKEALQIREKIPEKYLQFPHNLSNL 60  
 QY 61 DRIFDKTPEP 70  
 DB 61 DRIFDKTPEP 70  
 RESULT 9  
 AAB18686  
 ID AAB18686 standard; peptide; 70 AA.  
 XX  
 AC AAB18686;  
 XX  
 XX 22-JAN-2001 (first entry)  
 XX  
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 XX Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 24 /note= "wild type residue replaced with Leu"  
 FT Misc-difference 25 /note= "wild type residue replaced with Leu"  
 FT Misc-difference 26 /note= "wild type residue replaced with Leu"  
 FT Misc-difference 26 /note= "wild type residue replaced with Leu"  
 XX  
 XX WO200054573-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 XX 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX

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XX
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX
XX PS Claim 53; Page 46; 73pp; English.
XX
XX CC The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX SQ Sequence 70 AA;
XX
XX Query Match 92.8%; Score 335; DB 21; Length 70;
XX Best Local Similarity 92.9%; Pred. No. 1.7e-34;
XX Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 TLVWGEAAVDGRSARGCGQTSNDAAALNASSKEEALQIIREKIPKYLQFQHNLSNL 60
XX DB 1 TLVWGEFQVDRSARGCGQTSNDLLLEALNASSKEEALQIIREKIPKYLQFQHNLSNL 60
XX
XX QY 61 DRIFDKTPEP 70
XX DB 61 DRIFDKTPEP 70
XX
XX RESULT 10
XX AAB18689
XX ID AAB18689 standard; peptide; 70 AA.
XX AC AAB18689;
XX
XX DT 22-JAN-2001 (first entry)
XX
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 22 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX
XX FN WO200054573-A1.
XX
XX PD 21-SEP-2000.
XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX
XX

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PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX
XX PS Disclosure; Page 48-49; 73pp; English.
XX
XX CC The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX SQ Sequence 70 AA;
XX
XX Query Match 92.5%; Score 334; DB 21; Length 70;
XX Best Local Similarity 94.3%; Pred. No. 2.2e-34;
XX Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 TLVWGEAAVDGRSARGCGQTSNDAAALNASSKEEALQIIREKIPKYLQFQHNLSNL 60
XX DB 1 TLVWGEFQVDRSARGCGQTSAAAALNASSKEEALQIIREKIPKYLQFQHNLSNL 60
XX
XX QY 61 DRIFDKTPEP 70
XX DB 61 DRIFDKTPEP 70
XX
XX RESULT 11
XX AAB18680
XX ID AAB18680 standard; peptide; 70 AA.
XX AC AAB18680;
XX
XX DT 22-JAN-2001 (first entry)
XX
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 42 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 43 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 44 /note= "wild type residue replaced with Ala"
XX
XX FN WO200054573-A1.
XX
XX PD 21-SEP-2000.
XX
XX PF 15-MAR-2000; 2000WO-US06759.
XX

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PN WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX -
XX Claim 52; Page 44; 73pp; English.
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance to geminivirus infection in the
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX Sequence 70 AA;
XX Query Match 91.1%; Score 329; DB 21; Length 70;
XX Best Local Similarity 92.9%; Pred. No. 9.5e-34;
XX Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 TLVGEAAVDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGEFQVDRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 DRIFDKTPEP 70
RESULT 14
AAB18683
XX AAB18683 standard; peptide; 70 AA.
XX AC AAB18683;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX OS Tomato golden mosaic virus.
XX Key Location/Qualifiers
XX FT Misc-difference 59 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 61 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 61 /note= "wild type residue replaced with Ala"

FT Misc-difference 62 /note= "wild type residue replaced with Ala"
XX WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX -
XX Claim 53; Page 45; 73pp; English.
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance to geminivirus infection in the
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX Sequence 70 AA;
XX Query Match 90.9%; Score 328; DB 21; Length 70;
XX Best Local Similarity 92.9%; Pred. No. 1.3e-33;
XX Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 TLVGEAAVDGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Db 1 TLVWGEFQVDRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
Qy 61 DRIFDKTPEP 70
Db 61 AAFDKTPEP 70
RESULT 15
AAB18682
XX AAB18682 standard; peptide; 70 AA.
XX AC AAB18682;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX OS Tomato golden mosaic virus.
XX Key Location/Qualifiers
XX FT Misc-difference 52

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-52

Query Match      59.8%; Score 216; DB 3; Length 353;
Best Local Similarity 58.6%; Pred. No. 6.6e-20;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVGEAAVDGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
   :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 110 TIWGQFQVDRSARGGQSSANDSYAKALNADSIETSLTILKEQPKDYVLQHHNIRSL 169
   :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 DRIFDKTPEP 70
   :||: ||||| |||||
Db 170 ERIFFKVPEP 179
   :||: ||||| |||||

RESULT 5
US-08-838-151A-55
; Sequence 55, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-2

Query Match      59.8%; Score 216; DB 3; Length 359;
Best Local Similarity 56.5%; Pred. No. 6.7e-20;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVNGEAAVDGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 61
   :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 111 LEWGTQIDGRSARGGQTSNDAYAKAINAGSKQALDVIKELAPRDYVLHFNHNSNLD 170
   :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 62 RIFDKTPEP 70
   :||: ||||| |||||
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Db 171 KVFQVPPAP 179

## RESULT 7

US-08-809-103B-4  
; Sequence 4, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR95/01192  
; FILING DATE: 15-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-809-103B-4

Query Match 59.8%; Score 216; DB 3; Length 359;

Best Local Similarity 56.5%; Pred. No. 6.7e-20;

Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEAAVDCRSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 61  
Db 111 LEWGTFTQIDGRSARGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNINSNLD 170

QY 62 RIFDKTPEP 70

Db 171 KVFQVPPAP 179

## RESULT 8

US-08-809-103B-6  
; Sequence 6, Application US/08809103B  
; Patent No. 6133505  
; GENERAL INFORMATION:  
; APPLICANT: GRONENBORN, Bruno  
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94.11040  
; FILING DATE: 15-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR95/01192  
; FILING DATE: 15-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-809-103B-6

Query Match 59.8%; Score 216; DB 3; Length 359;

Best Local Similarity 56.5%; Pred. No. 6.7e-20;

Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEAAVDCRSARGGCGTNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 61  
Db 111 LEWGTFTQIDGRSARGGCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFNINSNLD 170

QY 62 RIFDKTPEP 70

Db 171 KVFQVPPAP 179

## RESULT 9

US-08-809-103B-8

; Sequence 8, Application US/08809103B

; Patent No. 6133505

; GENERAL INFORMATION:

; APPLICANT: GRONENBORN, Bruno

; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT

; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: YOUNG & THOMPSON

; STREET: 745 South 23rd Street

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/809,103B

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; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8
;
; Query Match 59.8%; Score 216; DB 3; Length 359;
; Best Local Similarity 56.5%; Pred. No. 6.7e-20;
; Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;
;
QY 2 LVWGEAAVDGSRGCGCOTSDNDAABALNASSKEALQIIRKIPKYLFOFHNLSNLD 61
DB 111 LEWGTFOIDGRSARGGQQTANDAYAKAINAGSKQALDVIKELAPRDYVLHFNHNSNLD 170
QY 62 RIFDKTPRP 70
DB 171 KVFQVPAP 179

RESULT 10
US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiivir
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460

```

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-2
;
; Query Match 59.3%; Score 214; DB 3; Length 361;
; Best Local Similarity 55.7%; Pred. No. 1.2e-19;
; Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;
;
QY 1 TLVWGEAAVDGSRGCGCOTSDNDAABALNASSKEALQIIRKIPKYLFOFHNLSN 60
DB 110 TIWGDFOIDGRSARGGQQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNSN 169
QY 61 DRIFDKTPRP 70
DB 170 ERIFAKAPEP 179

RESULT 11
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiivir
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4
;
; Query Match 59.3%; Score 214; DB 3; Length 361;
; Best Local Similarity 55.7%; Pred. No. 1.2e-19;
; Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;
;
QY 1 TLVWGEAAVDGSRGCGCOTSDNDAABALNASSKEALQIIRKIPKYLFOFHNLSN 60
DB 110 TIWGDFOIDGRSARGGQQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNSN 169

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;
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-24

Query Match      58.7%; Score 212; DB 3; Length 357;
Best Local Similarity 65.6%; Pred. No. 2.2e-19;
Matches 40; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY      4 WGEAAVDGSRARGGCGTSDNDAAAEALNASSKEEALQIREKIPEKYLFQFHNLSNLDRI 63
Db      111 FGVSIQDGRSARGGQGSANDAYAEALNSGSKSEALNILEKAPKDYILOFHNLSNLDRI 170

QY      64 F 64
Db      171 F 171

Search completed: December 23, 2003, 08:59:35
Job time : 11.6667 secs

;
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-24

Query Match      58.7%; Score 212; DB 3; Length 357;
Best Local Similarity 65.6%; Pred. No. 2.2e-19;
Matches 40; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY      4 WGEAAVDGSRARGGCGTSDNDAAAEALNASSKEEALQIREKIPEKYLFQFHNLSNLDRI 63
Db      111 FGVSIQDGRSARGGQGSANDAYAEALNSGSKSEALNILEKAPKDYILOFHNLSNLDRI 170

QY      64 F 64
Db      171 F 171

RESULT 15
US-08-838-151A-27
; Sequence 27, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-27
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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:59:44 ; Search time 76 Seconds

(without alignments)  
172.015 Million cell updates/sec

Title: US-09-289-346B-8

Perfect score: 361

Sequence: 1 TLVWGEAAVDRSARGGCQT.....POFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361	100.0	70	10	US-09-289-346A-8
2	350	97.0	70	10	US-09-289-346A-1
3	350	97.0	356	10	US-09-289-346A-11
4	342	94.7	70	10	US-09-289-346A-9
5	339	93.9	70	10	US-09-289-346A-12
6	338	93.6	70	10	US-09-289-346A-16
7	336	93.1	70	10	US-09-289-346A-14
8	335	92.8	70	10	US-09-289-346A-2
9	335	92.8	70	10	US-09-289-346A-10
10	334	92.5	70	10	US-09-289-346A-13
11	332	92.0	70	10	US-09-289-346A-4
12	332	92.0	70	10	US-09-289-346A-15
13	329	91.1	70	10	US-09-289-346A-5
14	328	90.9	70	10	US-09-289-346A-7
15	326	90.3	70	10	US-09-289-346A-6

16	318	88.1	70	10	US-09-289-346A-3
17	68.5	19.0	1713	15	US-10-171-311-113
18	66.5	18.4	512	12	US-10-301-661A-4
19	65	18.0	293	15	US-10-151-336-3
20	65	18.0	335	15	US-10-151-336-6
21	63.5	17.6	447	9	US-09-989-722-369
22	63.5	17.6	447	9	US-09-989-723-369
23	63.5	17.6	447	9	US-09-989-279-369
24	63.5	17.6	447	9	US-09-989-727-369
25	63.5	17.6	447	10	US-09-989-731-369
26	63.5	17.6	447	10	US-09-989-732-369
27	63.5	17.6	447	10	US-09-991-073-369
28	63.5	17.6	447	10	US-09-990-442-369
29	63.5	17.6	447	10	US-09-991-163-369
30	63.5	17.6	447	10	US-09-993-604-369
31	63.5	17.6	447	10	US-09-990-456-369
32	63.5	17.6	447	10	US-09-989-721-369
33	63.5	17.6	447	10	US-09-992-598-369
34	63.5	17.6	447	10	US-09-989-293A-369
35	63.5	17.6	447	10	US-09-989-735-369
36	63.5	17.6	447	10	US-09-990-444-369
37	63.5	17.6	447	10	US-09-991-181-369
38	63.5	17.6	447	10	US-09-989-730-369
39	63.5	17.6	447	10	US-09-990-436-369
40	63.5	17.6	447	11	US-09-993-687-369
41	63.5	17.6	447	11	US-09-989-734-369
42	63.5	17.6	447	11	US-09-997-653-369
43	63.5	17.6	447	11	US-09-993-667-369
44	63.5	17.6	447	11	US-09-997-428-369
45	63.5	17.6	447	11	US-09-997-666-369

ALIGNMENTS

RESULT 1

US-09-289-346A-8  
; Sequence 8, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruijssem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (7)..(8)  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine  
; OTHER INFORMATION: replacements (FQ118->AAl18).

Query Match	100.0%	Score 361;	DB 10;	Length 70;
Best Local Similarity	100.0%	Pred. No. 3.3e-36;		
Matches	70;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
QY	1	TLVWGEAAVDRSARGGCQTSNDAAALNASSKEALQIIREKIPKYLQFHNLSNL	60	
Db	1	TLVWGEAAVDRSARGGCQTSNDAAALNASSKEALQIIREKIPKYLQFHNLSNL	60	
QY		61 DRIFDKTPEP	70	

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Db      61 DRIFDKTPEP 70
|||||
110 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 169

QY      61 DRIFDKTPEP 70
|||||
170 DRIFDKTPEP 179

RESULT 4
US-09-289-346A-9
; Sequence 9, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (D120->A120)
US-09-289-346A-9

Query Match      94.7%; Score 342; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 8.5e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TLVWGEAAVDGRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
|||||
Db      1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60

QY      61 DRIFDKTPEP 70
|||||
Db      61 DRIFDKTPEP 70

RESULT 5
US-09-289-346A-12
; Sequence 12, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-12

Query Match      93.9%; Score 339; DB 10; Length 70;

Db      61 DRIFDKTPEP 70
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110 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 169

QY      61 DRIFDKTPEP 70
|||||
170 DRIFDKTPEP 179

RESULT 2
US-09-289-346A-1
; Sequence 1, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-1

Query Match      97.0%; Score 350; DB 10; Length 70;
Best Local Similarity 97.1%; Pred. No. 8.2e-37;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TLVWGEAAVDGRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
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Db      1 TLVWGEFQVDRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60

QY      61 DRIFDKTPEP 70
|||||
Db      61 DRIFDKTPEP 70

RESULT 3
US-09-289-346A-11
; Sequence 11, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (354)
; OTHER INFORMATION: Unsure about sequence assignment
US-09-289-346A-11

Query Match      97.0%; Score 350; DB 10; Length 356;
Best Local Similarity 97.1%; Pred. No. 6.8e-36;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TLVWGEAAVDGRSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFPHNLNSNL 60
|||||
```

Best Local Similarity 94.3%; Pred. No. 2e-35;  
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGGCOTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
|||||  
Db 1 TLVWGEFQVDGRSARGGCOTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
|||||  
QY 61 DRIFDKTPEP 70  
|||||  
Db 61 DRIFDKTPEP 70  
|||||

## RESULT 6

US-09-289-346A-16  
; Sequence 16, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
US-09-289-346A-16

Query Match 93.6%; Score 338; DB 10; Length 70;  
Best Local Similarity 94.3%; Pred. No. 2.7e-35;  
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGGCOTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
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Db 1 TLVWGEFQVDGRSARGGCOTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
|||||  
QY 61 DRIFDKTPEP 70  
|||||  
Db 61 DRIFDKTPEP 70  
|||||

## RESULT 7

US-09-289-346A-14  
; Sequence 14, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
US-09-289-346A-14

Query Match 93.1%; Score 336; DB 10; Length 70;  
Best Local Similarity 94.3%; Pred. No. 4.9e-35;

Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 TLVWGEAAVDGRSARGGCOTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
|||||  
Db 1 TLVWGEFQVDGRSARGGCOTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
|||||  
QY 61 DRIFDKTPEP 70  
|||||  
Db 61 DRIFDKTPEP 70  
|||||

## RESULT 8

US-09-289-346A-2  
; Sequence 2, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; NAME/KEY: VARIANT  
; LOCATION: (12) ..(15)  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TMV Rep  
; OTHER INFORMATION: Protein (aa 110-179) with alanine  
; OTHER INFORMATION: replacement (RSAR125->AAAA125).  
US-09-289-346A-2

Query Match 92.8%; Score 335; DB 10; Length 70;  
Best Local Similarity 92.9%; Pred. No. 6.5e-35;  
Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGGCOTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
|||||  
Db 1 TLVWGEFQVDGAAAGGCOTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60  
|||||  
QY 61 DRIFDKTPEP 70  
|||||  
Db 61 DRIFDKTPEP 70  
|||||

## RESULT 9

US-09-289-346A-10  
; Sequence 10, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/125,004  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 70  
; TYPE: PRT

```
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)...(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAAI36->LLLI36).
US-09-289-346A-10

Query Match          92.8%; Score 335; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 6.5e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGEAAVDGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TLVWGEFQVDCRSARGGCGQTSNDLLLEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

Qy 61 DRIFDKTPEP 70
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1993-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-13

Query Match          92.5%; Score 334; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 8.8e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TLVWGEAAVDGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TLVWGEFQVDCRSARGGCGQTSAAAALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

Qy 61 DRIFDKTPEP 70
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-4
; Sequence 4, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1993-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; NAME/KEY: VARIANT
; LOCATION: (42)...(44)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REKI54->AAAI54).
US-09-289-346A-4

Query Match          92.0%; Score 332; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.6e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGEAAVDGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TLVWGEFQVDCRSARGGCGQTSNDAAAEALNASSKEEALQIIRAAAIPEKYLQFHNLSNL 60

Qy 61 DRIFDKTPEP 70
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match          92.0%; Score 332; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.6e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLVWGEAAVDGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TLVWGEFQVDCRSARGGCGQTSNDAAAEALNASSAAALQIIREKIPEKYLQFHNLSNL 60

Qy 61 DRIFDKTPEP 70
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
```



```
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (47)..(49)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (SKY159->AAA159).
US-09-289-346A-5

Query Match          91.1%; Score 329; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 3.8e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLFPQFHNLSNL 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TLVWGEFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLFPQFHNLSNL 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 DRIFDKTPEP 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 DRIFDKTPEP 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-09-289-346A-7
; Sequence 7, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (59)..(62)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (NLDRI72->ALAA172).
US-09-289-346A-7

Query Match          90.9%; Score 328; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 5e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLFPQFHNLSNL 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TLVWGEFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLFPQFHNLSNL 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 DRIFDKTPEP 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AAIIDKTPEP 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
RESULT 15
US-09-289-346A-6
; Sequence 6, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (52)..(55)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (QFHN165->AFPA165).
US-09-289-346A-6
```

```
Query Match          90.3%; Score 326; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 9e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLFPQFHNLSNL 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TLVWGEFQVDGRSARGCGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLFPQFHNLSNL 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 DRIFDKTPEP 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 DRIFDKTPEP 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: December 23, 2003, 09:43:31  
Job time : 77 secs

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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.7778 Seconds  
(without alignments)  
569.747 Million cell updates/sec

Title: US-09-289-346B-8

Perfect score: 361

Sequence: 1 TLVWGEAAVDGRSARGGCGT.....FQFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query %	Length	ID	Description
1	350	97.0	352	1	VAL1_TGMV	P03567 tomato gold
2	250	69.3	361	1	VAL1_PYMV	P27258 potato yell
3	237	65.7	358	1	VAL1_CLVK	P14982 cassava lat
4	237	65.7	358	1	VAL1_CLVN	P14972 cassava lat
5	230	63.7	362	1	VAL1_TYLC	P36279 tomato yell
6	223	61.8	359	1	VAL1_TYLC	P38609 tomato yell
7	219	60.7	349	1	VAL1_PHV	P06923 pepper huas
8	216	59.8	359	1	VAL1_TYLC	P27260 tomato yell
9	214	59.3	353	1	VAL1_BGMV	P05175 bean golden
10	213	59.0	355	1	VAL1_BGMV	P21947 abutilon mo
11	212	58.7	357	1	VAL1_TYLC	P27259 tomato yell
12	210	58.2	358	1	VAL1_BCTV	P14991 beet curly
13	210	58.2	361	1	VAL1_TMOV	P06657 tomato mott
14	117	32.4	347	1	VAL1_SLUC	P29048 squash leaf
15	68.5	19.0	1713	1	LM33_HUMAN	Q16787 homo sapient
16	65.5	18.1	298	1	OLG2_CHICK	Q90xb3 gallus gall
17	64.5	17.9	299	1	Y175_HELPJ	Q9zmq7 helicobacte
18	63.5	17.6	447	1	TBL2_HUMAN	Q9v4p3 homo sapien
19	63.5	17.6	1610	1	CCAD_MESAU	Q92244 mesocricetu
20	63.5	17.6	2161	1	CCAD_HUMAN	Q01868 homo sapien
21	63.5	17.6	2203	1	CCAD_RAT	P27732 rattus norv
22	62	17.2	295	1	VAL1_TYDV	P31617 tobacco yel
23	61	16.9	1502	1	CYP1_YEAST	P12351 saccharomyc
24	60	16.6	432	1	PROA_DEIRA	Q9rtcd9 deinococcus
25	60	16.6	447	1	CDSA_DROME	P56079 d phosphati
26	59.5	16.5	136	1	Y452_CABEL	O62250 caenorhabdi
27	59.5	16.5	299	1	Y175_HELPJ	P56112 helicobacte
28	59.5	16.5	476	1	DGRE_HUMAN	Q96df8 homo sapien
29	59.5	16.5	479	1	DGRE_MOUSE	O70279 mus musculu
30	59	16.3	640	1	DNAK_RHOMR	Q9wxb1 rhodothermu
31	59	16.3	747	1	YU20_MOUSE	Q9wv70 mus musculu
32	58.5	16.2	297	1	RPPV_RABVP	P06747 rabies viru
33	58.5	16.2	334	1	G3P_EACST	P00362 bacillus st

## RESULT 1

VAL1\_TGMV STANDARD; PRT; 352 AA.

AC P03567;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE AL1 protein.

GN AC1.

OS Tomato golden mosaic virus (TGMV).

OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

OX NCBI\_TaxID=10831;

RN [1]

RP SEQUENCE FROM N.A.

RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;

RT "Complete nucleotide sequence of the infectious cloned DNA components of tomato golden mosaic virus: potential coding regions and regulatory sequences.";

RL EMO J. 3:2197-2205(1984).

CC - SIMILARITY: BELONGS TO GEMINIVIRUS ALL PROTEIN FAMILY.

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CC ----- NOT\_ANNOTATED\_CDS.

DR EMBL; K02029; -; NOT\_ANNOTATED\_CDS.

DR PIR; A04170; QOCVLI.

DR InterPro; IPR001191; Gemini\_AL1.

DR Pfam; PF00799; Gemini\_AL1; 1.

DR PRINTS; PR00227; GEMCOATAL1.

DR ProDom; PD000736; Gemini\_AL1; 1.

RW ATP-binding.

FT NP BIND 223 230 ATP (POTENTIAL).

SQ SEQUENCE 352 AA; 40332 MW; C33C938E9644B4A4 CRC64;

Query Match 97.0%; Score 350; DB 1; Length 352;

Best Local Similarity 97.1%; Pred. No. 5.7e-32;

Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGGCGTSDNDAABALNASSKEALQIIREKIPKYLQFQHNLSNL 60

Db 111 TLVWGEFQVDGRSARGGCGTSDNDAABALNASSKEALQIIREKIPKYLQFQHNLSNL 170

QY 61 DRIFDKTPEP 70

Db 171 DRIFDKTPEP 180

RESULT 2

VAL1\_PYMV

ID VAL1\_PYMV STANDARD; PRT; 361 AA.

AC P27258;

P15115 bacillus co  
P28868 candida alb  
Q82064 anabaena sp  
P45221 haemophilus  
O94751 schizosacch  
P42338 homo sapien  
Q99735 staphylococ  
Q8num9 staphylococ  
P36682 escherichia  
P49052 bacillus li  
Q8dfj1 vibrio vuln  
Q9cfig7 lactococcus

34 58.5 16.2 335 1 G3P\_BACCO  
35 58.5 16.2 428 1 GBA1\_CANAL  
36 58.5 16.2 491 1 AMPA\_ANASP  
37 58.5 16.2 589 1 YB67\_HABIN  
38 58.5 16.2 1044 1 BUB1\_SCHPO  
39 58.5 16.2 1070 1 FLIB\_HUMAN  
40 58 16.1 319 1 LDH2\_STAAM  
41 58 16.1 319 1 LDH2\_STAAM  
42 58 16.1 617 1 YACH\_ECOLI  
43 58 16.1 874 1 SLAP\_BACLI  
44 57.5 15.9 259 1 FLGH\_VIBVU  
45 57.5 15.9 439 1 XYLA\_LACIA

## ALIGNMENTS

```
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus.";
RL J. Gen. Virol. 72:1515-1520(1991).
CC -/- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; D00940; BAA00782.1; -.
DR PIR; J00364; Q0CVPT.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
KW NP_BIND
FT NP_BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;

Query Match 69.3%; Score 250; DB 1; Length 361;
Best Local Similarity 68.1%; Pred. No. 1e-20;
Matches 47; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGAAVDGRSARGCGQTSDAAAEALNASKEALQIIREKIPKYLQFPHNLSNL 60
Db 110 TIWGLFQIDGRSARGCGQTSDAAAEALNASKEALQIIREKIPKYLQFPHNLSNL 169
QY 61 DRIFDKTPE 69
Db 170 DRIFDKAPE 178

RESULT 3
VAL1 CLVK
ID VAL1 CLVK STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN ACl.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RX Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
CC -/- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
KW NP_BIND
FT NP_BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753EB92D69 CRC64;

Query Match 65.7%; Score 237; DB 1; Length 358;
Best Local Similarity 61.4%; Pred. No. 3e-19;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGAAVDGRSARGCGQTSDAAAEALNASKEALQIIREKIPKYLQFPHNLSNL 60
Db 109 TVEWGQFQIDGRSARGCGQTSDAAAEALNASKEALQIIREKIPKYLQFPHNLSNL 168
QY 61 DRIFDKTPE 70
Db 169 DRIFQBPAP 178

RESULT 4
VAL1 CLVN
ID VAL1 CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (40.4 kDa protein).
GN ACl.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
RL Nucleic Acids Res. 18:197-198(1990).
CC -/- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; X17095; CAA34953.1; -.
DR PIR; S07594; S07594.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
DR ATP-binding.
KW NP_BIND
FT NP_BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16BB0CB2D5E2C CRC64;

Query Match 65.7%; Score 237; DB 1; Length 358;
Best Local Similarity 61.4%; Pred. No. 3e-19;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVWGAAVDGRSARGCGQTSDAAAEALNASKEALQIIREKIPKYLQFPHNLSNL 60
Db 109 TVEWGQFQIDGRSARGCGQTSDAAAEALNASKEALQIIREKIPKYLQFPHNLSNL 168
QY 61 DRIFDKTPE 70
Db 169 DRIFQBPAP 178
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CC      EMBL; Z25751; CAA81026.1; -.
DR      PIR; S39211; S39211.
DR      InterPro; IPR001191; Gemini_AL1.
DR      Pfam; PF00799; Gemini_AL1.
DR      PRINTS; PR00227; GEMCOATL1.
DR      ProDom; PD000736; Gemini_AL1; 1.
KW      ATP-binding.
FT      NP BIND 221 228 ATP (POTENTIAL).
SQ      SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3BC CRC64;

Query Match 61.8%; Score 223; DB 1; Length 359;
Best Local Similarity 59.4%; Pred. No. 1.1e-17;
Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY      2 LVWGEAAVDGRSARGGCGTSDNDAALNASSKEALQIIRKIPKYLQFHNLSNLD 61
DB      111 LEWTFQIDGRSARGGCGTSDNDAALNASSKEALQIIRKIPKYLQFHNLSNLD 170
QY      62 RIFDKTPEP 70
DB      171 RVFQVPPAP 179

RESULT 7
VAL1 PHUV
ID VAL1 PHUV STANDARD; PRT; 349 AA.
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AL1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
RN [1]__TaxID=28349;
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
RT comparison with bipartite geminiviruses.";
RL J. Gen. Virol. 74:2225-2231(1993).
CC -/- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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-----
DR      EMBL; X70418; CAA49856.1; -.
DR      PIR; J02300; J02300.
DR      PIR; S31875; S31875.
DR      InterPro; IPR001191; Gemini_AL1.
DR      Pfam; PF00799; Gemini_AL1; 1.
DR      PRINTS; PR00227; GEMCOATL1.
DR      ProDom; PD000736; Gemini_AL1; 1.
KW      ATP-binding.
FT      NP BIND 221 228 ATP (BY SIMILARITY).
SQ      SEQUENCE 349 AA; 39722 MW; D5F4E76CD56370P4 CRC64;

Query Match 60.7%; Score 219; DB 1; Length 349;
Best Local Similarity 58.6%; Pred. No. 3e-17;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY      1 TLVWGEAAVDGRSARGGCGTSDNDAALNASSKEALQIIRKIPKYLQFHNLSNLD 60
DB      110 TVWGEFQIDGRSARGGCGTSDNDAALNASSKEALQIIRKIPKYLQFHNLSNLD 169

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CC      EMBL; Z25751; CAA81026.1; -.
DR      PIR; S39211; S39211.
DR      InterPro; IPR001191; Gemini_AL1.
DR      Pfam; PF00799; Gemini_AL1.
DR      PRINTS; PR00227; GEMCOATL1.
DR      ProDom; PD000736; Gemini_AL1; 1.
KW      ATP-binding.
FT      NP BIND 221 228 ATP (POTENTIAL).
SQ      SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3BC CRC64;

Query Match 63.7%; Score 230; DB 1; Length 362;
Best Local Similarity 54.1%; Pred. No. 1.8e-18;
Matches 46; Conservative 9; Mismatches 14; Indels 16; Gaps 1;

QY      1 TLVWGEAAVDGRSARGGCGTSDNDAALNASSKEALQIIRKIPKYLQFHNLSNLD 60
DB      110 TLWGEFQIDGRSARGGCGTSDNDAALNASSKEALQIIRKIPKYLQFHNLSNLD 169
QY      61 DRI-----PDKTPPE 69
DB      170 DRIFTPPEVYVSPFLSSSFDVRPE 194

RESULT 6
VAL1 TYLCA
ID VAL1 TYLCA STANDARD; PRT; 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 protein (CI protein).
GN CI.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
RN [1]__TaxID=37139;
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Norris E., Hidalgo E., Accotto G., Moriones E.;
RA "High similarity among the tomato yellow leaf curl virus isolates
RT from the west Mediterranean basin: the nucleotide sequence of an
RT infectious clone from Spain.";
RL Arch. Virol. 135:165-170(1994).
CC -/- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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QY 61 DRIFDKTPEP 70
Db 170 NRIFQTPPEP 179

RESULT 8
VAL1_TYLCM STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE AL1 protein (Cl protein).
GN Cl.
OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92107660; PubMed=1840676;
RA Khey-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
RA Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a
RT whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; M10070; AAA46318.1; -
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 59.8%; Score 216; DB 1; Length 359;
Best Local Similarity 56.5%; Pred. No. 6.8e-17;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEAAVDGRSGCGQTSNDAAAEALNASSKEEALQIREKIPKYLFOFHNLSNLD 61
Db 111 LEWGTFOIGRSARGGQQTANDAYAKAINAGSKQALDVIKELAPRDYVLHFNHNSNLD 170
QY 62 RIFDKTPEP 70
Db 171 KVFQVPEP 179

RESULT 9
VAL1_BGMV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE AL1 protein (40.2 kDa protein).
GN AC1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimmatt G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; X15983; -; NOT_ANNOTATED_CDS.
DR PIR; A36214; QOCVWL.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.

SEQUENCE FROM N.A.
RA Howarth A.J., Caton J., Bossert M., Goodman R.M.;
RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
RT regulation in geminiviruses";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; M10070; AAA46318.1; -
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 59.3%; Score 214; DB 1; Length 353;
Best Local Similarity 58.6%; Pred. No. 1.1e-16;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLWGEAAVDGRSGCGQTSNDAAAEALNASSKEEALQIREKIPKYLFOFHNLSNLD 60
Db 110 TIEWGQPVQGRSGGQGSANDYAKALNADSIESALTILKBEQPKDYVLQNHNSNLD 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFFKVPEP 179

RESULT 10
VAL1_ABMV STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.
GN AC1.
OS Abutilon mosaic virus (isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91020984; PubMed=2219703;
RA Frischmuth T., Zimmatt G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; X15983; -; NOT_ANNOTATED_CDS.
DR PIR; A36214; QOCVWL.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.

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FT NP BIND      221      228      ATP (POTENTIAL).
SQ SEQUENCE    355 AA; 40257 MW; 16A2CA8A63251E95 CRC64;

Query Match
Best Local Similarity 59.0%; Score 213; DB 1; Length 355;
Matches 40; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 1 TLVWGGAADVGRSARGGQTSNDAAALNASSKEALQIREKIPKYLFOFHNLSNL 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TLWGFQIDGRSARGGQTSNDAAALNASSKEALQIREKIPKYLFOFHNLSNL 169
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DRIFDKTPEP 70
   :|||:|||||
Db 170 ERIFAKAPEP 179
   :|||:|||||

RESULT 11
VAL1_TYLCV
ID VAL1_TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Ali protein (C1 protein).
GN C1.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9204070; PubMed=1926771;
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
   with a single genomic component.";
RL Virology 185:151-161(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
CC
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CC
CC EMBL; X15656; CAA33688.1; -.
CC PIR; D40779; QQCVC1.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND      219      226      ATP (POTENTIAL).
SQ SEQUENCE    357 AA; 40678 MW; 939AB6BE1AB3B2A7 CRC64;

Query Match
Best Local Similarity 58.7%; Score 212; DB 1; Length 357;
Matches 40; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 4 WGAADVGRSARGGQTSNDAAALNASSKEALQIREKIPKYLFOFHNLSNLDRI 63
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 111 FGVSQIDGRSARGGQTSNDAAALNASSKEALQIREKIPKYLFOFHNLSNLDRI 170
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 64 F 64
   |
Db 171 F 171
   |

RESULT 12
VAL1_BCTV
ID VAL1_BCTV STANDARD; PRT; 358 AA.
AC P14991;
DT 01-APR-1990 (Rel. 14, Created)

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DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Ali protein (40.8 kDa protein).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
   beet curly top virus."
RL EMBL J. 5:1761-1767(1986).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
CC
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CC
CC EMBL; X04144; -. NOT ANNOTATED CDS.
CC InterPro; IPR001191; Gemini_AL1.
CC Pfam; PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND      222      229      ATP (POTENTIAL).
SQ SEQUENCE    358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;

Query Match
Best Local Similarity 58.2%; Score 210; DB 1; Length 358;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGGAADVGRSARGGQTSNDAAALNASSKEALQIREKIPKYLFOFHNLSNL 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TLWGFQIDGRSARGGQTSNDAAALNASSKEALQIREKIPKYLFOFHNLSNL 169
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DRIFDKTPEP 70
   :|||:|||||
Db 170 QKIFQRPDP 179
   :|||:|||||

RESULT 13
VAL1_TMOV
ID VAL1_TMOV STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Ali protein.
GN AL1.
OS Tomato mottle virus (isolate Florida) (TMov).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93107858; PubMed=1469361;
RA Abouzid A.M., Polston J.E., Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
   isolated from tomatoes in Florida."
RL J. Gen. Virol. 73:3225-3229(1992).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL1 PROTEIN FAMILY.
CC
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CC

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DR EMBL; L14460; AAC32414.1; -.
DR PIR; JQ1870.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND. 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 8138B65CEAC6950 CRC64;

Query Match 58.2%; Score 210; DB 1; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.3e-16;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLVGEAAVDRSGGCGQTSDNAAAEALNASSKEEALQIREKIPEKYLQFHNLSNL 60
Db 110 TIEMDFQIDGRSARGGQSANDSYAKALNAGSVQSALAVLREBPQKDFVLQHNIRSL 169

Qy 61 DRIPDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 14
ID VAL1_SLCV STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE AL1 protein.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G.; Lazdins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic components of a bipartite squash leaf curl geminivirus with a broad host range phenotype.";
RT Virology 180:58-69(1991).
RL Virology 180:58-69(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; M38183; AAC32410.1; ALT_INIT.
DR PIR; C36785; QOCVSI.
DR InterPro; IPR001191; Gemini AL1.
DR Pfam; PF00799; Gemini AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP BIND. 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDAEBDD122110E CRC64;

Query Match 32.4%; Score 117; DB 1; Length 347;
Best Local Similarity 37.9%; Pred. No. 9e-06;
Matches 25; Conservative 12; Mismatches 25; Indels 4; Gaps 1;

Qy 5 GEAAVDRSGGCGQTSDNAAAEALNASSKEEALQIREKIPEKYLQFHNLSNDRIF 64
Db 116 GQYKVSQ-----GSKSNKDDVYHNAVAGSAGEALDIKAGPKTFVYVNNLLANVELP 171

Qy 65 DKTPPEP 70
Db 172 QKPEPEP 177
```

## RESULT 15

```
ID LAM3_HUMAN STANDARD; PRT; 1713 AA.
AC Q16787; Q13679; Q13680;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Laminin alpha-3 chain precursor (Epiligrin 170 kDa subunit) (E170)
DE (Nicein alpha subunit).
GN LAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=keratinocytes;
RX MEDLINE=94357926; PubMed=8077230;
RA Ryan M.C.; Tizard R.; Vandevanter D.R.; Carter W.G.;
RT "Cloning of the LAM3 gene encoding the alpha 3 chain of the adhesive ligand epiligrin. Expression in wound repair.";
RT J Biol. Chem. 269:22779-22787(1994).
RL [2]
RP SEQUENCE OF 1-1331 FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=96163880; PubMed=8586427;
RA Vidal F.; Baudoin C.; Miquel C.; Galliano M.-P.; Christiano A.M.;
RA Utito J.; Ortonne J.-P.; Meneguzzi G.;
RT "Cloning of the laminin alpha 3 chain gene (LAM3) and identification of a homozygous deletion in a patient with Herlitz junctional epidermolysis bullosa.";
RT Genomics 30:273-280(1995).
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.
CC -1- FUNCTION: LAMININ-5 IS THOUGHT TO BE INVOLVED IN (1) CELL ADHESION VIA INTEGRIN ALPHA-3/BETA-1 IN FOCAL ADHESION AND INTEGRIN ALPHA-6/BETA-4 IN HEMIDESMOSOMES, (2) SIGNAL TRANSDUCTION VIA TYROSINE PHOSPHORYLATION OF PPI25-FAK AND P80, (3) DIFFERENTIATION OF KERATINOCYTES.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end. The alpha-3 chain is a subunit of laminin-5 (epiligrin/kalinin/nicein), and possibly also a component of laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).
CC -1- ALTERNATIVE PRODUCTS:
CC Name=A;
CC IsoId=Q16787-1; Sequence=Displayed;
CC Name=B;
CC IsoId=Q16787-2; Sequence=VSP_003037;
CC Note=Sequence incomplete;
CC -1- TISSUE SPECIFICITY: SKIN; RESPIRATORY, URINARY, AND DIGESTIVE EPITHELIA AND IN OTHER SPECIALIZED TISSUES WITH PROMINENT SECRETORY OR PROTECTIVE FUNCTIONS. EPITHELIAL BASEMENT MEMBRANE, AND EPITHELIAL CELL TONGUE THAT MIGRATES INTO A WOUND BED. A DIFFERENTIAL AND FOCAL EXPRESSION OF THE ALPHA-3 CHAIN IS OBSERVED IN THE CNS.
CC -1- INDUCTION: LAMININ-5 IS UP-REGULATED IN WOUND SITES OF HUMAN SKIN.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- DOMAIN: DOMAIN G IS GLOBULAR.
CC -1- DISEASE: DEFECTS IN LAM3 ARE A CAUSE OF JUNCTIONAL EPIDERMOLYSIS BULLOSA (JEB) GRAVIS, ALSO KNOWN AS HERLITZ TYPE JEB. IT IS A BLISTERING DISORDER IN SKIN THAT IS CHARACTERIZED BY A SEPARATION OF BASAL CELLS FROM THE BASEMENT MEMBRANE DUE TO A DECREASED NUMBER OF HEMIDESMOSOMES. LAMININ-5 IS MISSING FROM THE BASEMENT
```





GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 25.3333 seconds  
(without alignments)  
713.040 Million cell updates/sec

Title: US-09-289-346b-8

Perfect score: 361

Sequence: 1 TLVWGEAAVDGRSARGGQT.....FQFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

SPTREMBL\_23.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_plant.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	301	83.4	351	Q91R10	Q91R10 tomato seve
2	299	82.8	352	Q9E000	Q9E000 tomato rugo
3	291	80.6	232	Q8QPV3	Q8QPV3 tomato chio
4	282	78.1	226	Q9WHF6	Q9WHF6 tomato mild
5	282	78.1	226	O09727	O09727 leonurus mo
6	280	77.6	361	Q67574	Q67574 bean golden
7	278	77.0	225	Q9QDB1	Q9QDB1 cowpea gold
8	278	77.0	314	Q9ELT8	Q9ELT8 sweet potat
9	278	77.0	364	Q9S855	Q9S855 sweet potat
10	275	76.2	185	Q9E693	Q9E693 sida golden
11	271	75.1	235	Q8QPU4	Q8QPU4 tomato infe
12	270	74.8	208	Q8JLY3	Q8JLY3 potato yell
13	270	74.8	289	Q8JLY5	Q8JLY5 potato yell
14	267	74.0	149	P88975	P88975 macroptiliu
15	267	74.0	233	Q9YLA4	Q9YLA4 macroptiliu
16	266	73.7	361	Q8JMJ4	Q8JMJ4 potato yell

17	264	73.1	360	12	Q8QMH4	Q8QMH4 sida mottle
18	262	72.6	361	12	Q8QVH0	Q8QVH0 ageratum en
19	261	72.3	234	12	Q3180	Q3180 geminivirid
20	259	71.7	223	12	Q8QPU7	Q8QPU7 tomato seve
21	258	71.5	190	12	Q9Z089	Q9Z089 tobacco lea
22	258	71.5	190	12	Q9Z084	Q9Z084 tobacco lea
23	257	71.2	190	12	Q9W827	Q9W827 tobacco lea
24	257	71.2	208	12	Q9Z0C4	Q9Z0C4 tobacco lea
25	257	71.2	359	12	Q91M88	Q91M88 tobacco lea
26	257	71.2	359	12	Q8JVE8	Q8JVE8 tomato curl
27	255	70.6	208	12	Q9Z0C0	Q9Z0C0 tobacco lea
28	255	70.6	208	12	Q9Z0B8	Q9Z0B8 tobacco lea
29	253	70.1	208	12	Q9Z0B6	Q9Z0B6 tobacco lea
30	252	69.8	203	12	Q9Z083	Q9Z083 tobacco lea
31	252	69.8	363	12	Q73577	Q73577 cotton leaf
32	247	68.4	359	12	Q91B86	Q91B86 ageratum ye
33	247	68.4	360	12	Q9DX10	Q9DX10 ageratum ye
34	245	67.9	208	12	Q9Z0A0	Q9Z0A0 tobacco lea
35	245	67.9	363	12	Q72719	Q72719 cotton leaf
36	245	67.9	363	12	Q72705	Q72705 cotton leaf
37	244	67.6	190	12	Q9Z086	Q9Z086 tobacco lea
38	244	67.6	208	12	Q9Z0C6	Q9Z0C6 tobacco lea
39	243	67.3	349	12	Q88888	Q88888 tomato pseu
40	243	67.3	362	12	O56816	O56816 chayote mos
41	242	67.0	359	12	Q9YZV4	Q9YZV4 tomato yell
42	242	67.0	359	12	Q9YUX7	Q9YUX7 tomato yell
43	242	67.0	359	12	Q9YL27	Q9YL27 tomato yell
44	242	67.0	359	12	Q9YZV2	Q9YZV2 tomato yell
45	242	67.0	362	12	Q8V0J1	Q8V0J1 cotton leaf

## ALIGNMENTS

## RESULT 1

Q91R10 PRELIMINARY; PRT; 351 AA.  
ID Q91R10  
AC Q91R10;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Rep protein.  
GN AC1.  
OS Tomato severe rugose virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=158463;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Minas Gerais;  
RA Rezende W.L., Goulart L.R., Parreira K.S., Figueiredo J.E.F.;  
RT "The full-length DNA-A nucleotide sequence of a novel tomato-infecting begomovirus, Tomato severe rugose virus, in Brazil.";  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY029750; AAK50357.1; -.  
DR InterPro; IPR001191; Gemini\_AL1.  
DR Pfam; PF00799; Gemini\_AL1; I.  
DR PRINTS; PR00227; GEMCOATL1.  
DR PRODOM; PD000736; Gemini\_AL1; I.  
SQ SEQUENCE 351 AA; 40122 MW; 87F937A4F873B6CF CRC64;

Query Match 83.4%; Score 301; DB 12; Length 351;  
Best Local Similarity 80.0%; Pred. No. 3.4e-26;  
Matches 56; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGGQTSDNAAALNASKEEALQIIRKIKPEKLFQFHNLNSL 60

Db 111 TIENGFEQIDGRSARGGCGTANDAAALNAPSQDVALQIIRKIKPEKLFQFHNLNSL 170

QY 61 DRIFDKTPEP 70

Db 171 DRIFARAPPEP 180



```

SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;
Query Match 78.1%; Score 282; DB 12; Length 226;
Best Local Similarity 78.6%; Pred. No. 3e-24;
Matches 55; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGCGCOTSDNAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
DB 111 TVWGEFQVDRSGSRGCGQTNDAAAEALNAPDKRTALQIIEKLPKYLFOFHNLSNL 170

QY 61 DRIFDKTPEP 70
DB 171 DRIFAKAPEP 180

RESULT 6
Q67574 PRELIMINARY; PRT; 361 AA.
AC Q67574;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative replicative protein.
GN ALI.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration.";
RL Phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RT "Differentiation of bean-infecting geminiviruses by nucleic acid
RT hybridization probes and aspects of bean golden mosaic in Brazil.";
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus.";
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M88686; AAA46312.1; -.
DR InterPro; IPR001191; Gemin_A11.
DR Pfam; PF00799; Gemin_A11; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemin_A11; 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 77.6%; Score 280; DB 12; Length 361;
Best Local Similarity 77.6%; Pred. No. 8.9e-24;
Matches 52; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 4 WGEAAVDGRSARGCGCOTSDNAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63
DB 113 WGFQVDRSGSRGCGQTNDAAAEALNASSKEEAMQIIEKLPKYLFOFHNLSNLDRI 172

QY 64 FDKTPEP 70
DB 173 FTKAPDP 179

RESULT 7
Q9QDB1 PRELIMINARY; PRT; 225 AA.
ID Q9QDB1
AC Q9QDB1;

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DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Replication associated protein (Fragment).
GN REF.
OS Cowpea golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGMV-BR;
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RT Brazil.";
RL Submitted (SRP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF188708; AAF06318.1; -.
DR InterPro; IPR001191; Gemin_A11.
DR Pfam; PF00799; Gemin_A11; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemin_A11; 1.
FT NON TER 225 225
SQ SEQUENCE 225 AA; 25766 MW; 1089CB6BD8D15BSD CRC64;

Query Match 77.0%; Score 278; DB 12; Length 225;
Best Local Similarity 77.6%; Pred. No. 8.5e-24;
Matches 52; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 WGEAAVDGRSARGCGCOTSDNAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNLDRI 63
DB 113 WGFQVDRSGSRGCGQTNDAAAEALNASSKEEAMQIIEKLPKYLFOFHNLSNLDRI 172

QY 64 FDKTPEP 70
DB 173 FKPPPEP 179

RESULT 8
Q9ELT8 PRELIMINARY; PRT; 314 AA.
ID Q9ELT8
AC Q9ELT8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Replication association protein.
GN ACL.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288227; AAG01006.1; -.
DR InterPro; IPR001191; Gemin_A11.
DR Pfam; PF00799; Gemin_A11; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemin_A11; 1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 77.0%; Score 278; DB 12; Length 314;
Best Local Similarity 80.9%; Pred. No. 1.3e-23;
Matches 55; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGRSARGCGCOTSDNAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
DB 110 TITWGEFQVDRSGSRGCGQTNDAAAEALNAGSKEEALQIIREKLPKYLFOFHNLSNL 169

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QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 9
Q9Q55 PRELIMINARY; PRT; 364 AA.
AC Q9Q55;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RN SEQUENCE FROM N.A.
RP Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257 (1998).
RN [2]
RN SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RT virus: nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0 (1999).
DR EMBL; AF104036; AAD47173.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 77.0%; Score 278; DB 12; Length 364;
Best Local Similarity 80.9%; Pred. No. 1.5e-23;
Matches 55; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGSRAGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
Db 110 TIWGFQIDGSRAGCGCQTANDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 169

QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN-Jamaica;
RA Royle M.E., McLaughlin W.A., Nakhla N.K., Maxwell D.P.;
RT "Genetic Diversity among geminiviruses associated with the weed
RT species Sida spp, Macroptilium lathyroides, and Wissadula amplissima
RT from Jamaica.";
RL Plant Dis. 81:1251-1258 (1997).
DR EMBL; U67926; AAB97865.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.

QY ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 185
SQ SEQUENCE 185 AA; 20975 MW; 3913850A025A5EE1 CRC64;

Query Match 76.2%; Score 275; DB 12; Length 185;
Best Local Similarity 71.4%; Pred. No. 1.5e-23;
Matches 50; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 TLVWGEAAVDGSRAGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
Db 89 TIWGFQIDGSRAGCGCQTANDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 148

QY 61 DRIFDKTP 70
Db 149 DRIFSKPP 158

RESULT 11
Q8QPU4 PRELIMINARY; PRT; 235 AA.
AC Q8QPU4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (fragment).
GN AC1.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=MG-B11;
RA Ribeiro S.G., Ambrozovicus L.P., de Avila A.C., Calegario R.F.,
RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049208; AAL82833.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON_TER 235
SQ SEQUENCE 235 AA; 26690 MW; 0FA9A3BE0DD9C810 CRC64;

Query Match 75.1%; Score 271; DB 12; Length 235;
Best Local Similarity 74.6%; Pred. No. 5.7e-23;
Matches 50; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 4 WGEAAVDGSRAGCGCOTSDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 63
Db 113 WGIFQIDGSRAGCGCQTANDAAAEALNASSKEALQIIREKIPEKYLFOFHNLSNL 172

QY 64 DRIFDKTP 70
Db 173 FTKAPDP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RN SEQUENCE FROM N.A.
RP Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

```

VA ;0101C=Q1YBI\_TGCM

Db

Db 170 DRIFMKDPEP 179

Search completed: December 23, 2003, 09:03:37  
Job time : 26.3333 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:19 ; Search time 32.6667 Seconds  
(without alignments)  
340.128 Million cell updates/sec

Title: US-09-289-346B-9

Perfect score: 362

Sequence: 1 TLVMEFQVAGSARGCQT.....FQHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*  
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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	362	100.0	70	21 AAB18685	Mutant peptide der
2	356	98.3	70	21 AAB18677	Peptide fragment f
3	356	98.3	356	21 AAB18687	Amino acid sequenc
4	345	95.3	70	21 AAB18688	Mutant peptide der
5	344	95.0	70	21 AAB18692	Mutant peptide der
6	342	94.5	70	21 AAB18684	Mutant peptide der
7	342	94.5	70	21 AAB18690	Mutant peptide der
8	341	94.2	70	21 AAB18678	Mutant peptide der
9	341	94.2	70	21 AAB18686	Mutant peptide der

10	340	93.9	70	21 AAB18689	Mutant peptide der
11	338	93.4	70	21 AAB18680	Mutant peptide der
12	338	93.4	70	21 AAB18691	Mutant peptide der
13	335	92.5	70	21 AAB18681	Mutant peptide der
14	334	92.3	70	21 AAB18683	Mutant peptide der
15	332	91.7	70	21 AAB18682	Mutant peptide der
16	324	89.5	70	21 AAB18679	Mutant peptide der
17	223.5	61.7	50	23 AAO22043	Retinoblastoma-bin
18	222	61.3	353	18 AAW34338	Bean golden mosaic
19	222	61.3	353	18 AAW34332	Bean golden mosaic
20	222	61.3	353	18 AAW34333	Bean golden mosaic
21	222	61.3	353	18 AAW34334	Bean golden mosaic
22	222	61.3	353	18 AAW34335	Bean golden mosaic
23	222	61.3	359	17 AAR88870	Sardinian tomato y
24	222	61.3	359	17 AAR88871	Sardinian tomato y
25	222	61.3	359	17 AAR88872	Sardinian tomato y
26	220	60.8	353	8 AAP70407	ORF 4 gene product
27	220	60.8	361	18 AAW34336	Tomato mottle viru
28	220	60.8	361	18 AAW34324	Tomato mottle viru
29	220	60.8	361	18 AAW34325	Tomato mottle viru
30	220	60.8	361	18 AAW34326	Tomato mottle viru
31	213.5	59.0	361	8 AAP70562	Product of ORF 4 f
32	208	57.5	362	19 AAW56495	Tobacco leaf curl
33	207	57.2	357	18 AAW34329	Tomato yellow leaf
34	207	57.2	357	18 AAW34330	Tomato yellow leaf
35	207	57.2	357	18 AAW34331	Tomato yellow leaf
36	199	55.0	357	18 AAW34337	Tomato yellow leaf
37	96	26.5	142	24 ABP58120	Tomato yellow leaf
38	77	21.3	857	23 ABP62804	Protein fragment #
39	70.5	19.5	945	22 ABB65231	Drosophila melanog
40	66.5	18.4	665	22 ABB70991	Drosophila melanog
41	65	18.0	232	21 AAY92317	Geminivirus Rep C1
42	65	18.0	335	21 AAY92318	Mastrevirus Rep in
43	64.5	17.8	299	18 AAW55450	H. pylori ORF 02ae
44	64.5	17.8	512	19 AAW68473	HIV-1 strain YBF30
45	62.5	17.3	447	21 AAY99659	Human GTPase assoc

## ALIGNMENTS

RESULT 1  
AAB18685  
ID AAB18685 standard; peptide; 70 AA.  
AC AAB18685;  
XX  
DT 22-JAN-2001 (first entry)  
XX  
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
XX  
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
ribosome binding region; resistance; geminivirus infection.  
XX  
OS Synthetic.  
OS Tomato golden mosaic virus.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 10 /note= "wild type residue replaced with Ala"  
XX  
FN WO200054573-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 15-MAR-2000; 2000WO-US06759.  
XX  
PR 18-MAR-1999; 99US-0125004.  
PR 09-APR-1999; 99US-0289346.  
XX  
PA (UYN)- UNIV NORTH CAROLINA STATE.  
XX  
PI Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

XX comprise a nucleic acid construct containing a nucleic acid sequence

XX encoding a mutant AL1 protein with a mutation in the Rb binding region

XX

XX Claim 53; Page 46; 73pp; English.

XX

XX The present sequence represents a mutant peptide, derived from a

XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds

XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded

XX DNA, and interacts with other viral and host proteins. Mutants of the AL1

XX protein are used to produce transgenic plants. The mutation in AL1 is

XX present in a ribosome binding region, and expression of mutant AL1

XX protein imparts increased resistance to geminivirus infection in the

XX plant. Mutant AL1 proteins are useful for producing plants having

XX increased resistance or reduced sensitivity to a geminivirus such as

XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian

XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper

XX virus, cotton leaf curl virus or beet curly top virus.

XX

SQ Sequence 70 AA;

Query Match 100.0%; Score 362; DB 21; Length 70;

Best Local Similarity 100.0%; Pred. No. 1.2e-37;

Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60

Db 1 TLVWGEFQVAGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70

Db 61 DRIFDKTPEP 70

RESULT 2

AAB18677

ID AAB18677 standard; peptide; 70 AA.

XX AAB18677;

XX 22-JAN-2001 (first entry)

XX Peptide fragment from Rep protein of TGMV (amino acids 110-179).

XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX ribosome binding region; resistance; geminivirus infection.

XX Tomato golden mosaic virus.

XX WO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

XX comprise a nucleic acid construct containing a nucleic acid sequence

XX encoding a mutant AL1 protein with a mutation in the Rb binding region

XX

PT

XX Disclosure; Page 18; 73pp; English.

XX

XX The present sequence is derived from a geminivirus replication (Rep)

XX protein, which is also known as AL1. AL1 binds double-stranded DNA,

XX catalyzes cleavage and ligation of single-stranded DNA, and interacts

XX with other viral and host proteins. Mutants of the AL1 protein are used

XX to produce transgenic plants. The mutation in AL1 is present in a

XX ribosome binding region, and expression of mutant AL1 protein imparts

XX increased resistance to geminivirus infection in the plant. Mutant AL1

XX proteins are useful for producing plants having increased resistance or

XX reduced sensitivity to a geminivirus such as tomato golden mosaic virus,

XX tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl

XX virus, African cassava mosaic virus, Indian cassava mosaic virus, potato

XX yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,

XX squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or

XX beet curly top virus.

XX

SQ Sequence 70 AA;

Query Match 98.3%; Score 356; DB 21; Length 70;

Best Local Similarity 98.6%; Pred. No. 6.6e-37;

Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60

Db 1 TLVWGEFQVAGRSARGGQTSNDAAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70

Db 61 DRIFDKTPEP 70

RESULT 3

AAB18687

ID AAB18687 standard; peptide; 356 AA.

XX AAB18687;

XX 22-JAN-2001 (first entry)

XX Amino acid sequence of a geminivirus replication protein of TGMV.

XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX ribosome binding region; resistance; geminivirus infection.

XX Tomato golden mosaic virus.

XX Key Location/Qualifiers

XX Misc-difference 354 /note= "unspecified amino acid"

XX WO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

XX comprise a nucleic acid construct containing a nucleic acid sequence

XX encoding a mutant AL1 protein with a mutation in the Rb binding region

XX



PS Disclosure; Page 47-48; 73pp; English.

XX The present sequence represents a geminivirus replication (Rep)  
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,  
 CC catalyses cleavage and ligation of single-stranded DNA, and interacts  
 CC with other viral and host proteins. Mutants of the AL1 protein are used  
 CC to produce transgenic plants. The mutation in AL1 is present in a  
 CC ribosome binding region, and expression of mutant AL1 protein imparts  
 CC increased resistance to geminivirus infection in the plant. Mutant AL1  
 CC proteins are useful for producing plants having increased resistance or  
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,  
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl  
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato  
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,  
 CC squash leaf curl virus, Texas golden mosaic virus, cotton leaf curl virus or  
 CC beet curly top virus.

XX Sequence 356 AA;

Query Match 98.3%; Score 356; DB 21; Length 356;  
 Best Local Similarity 98.6%; Pred. No. 5.1e-36;  
 Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLVWGFQVAGRSARGCGCTSDNDAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60  
 |||||  
 DB 110 TLVWGFQVAGRSARGCGCTSDNDAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 169  
 |||||  
 QY 61 DRIFDKTPEP 70  
 |||||  
 DB 170 DRIFDKTPEP 179  
 |||||

#### RESULT 4

AAAB18688  
 ID AAB18688 standard; peptide; 70 AA.

XX AAB18688;

XX 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX Synthetic.

OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 19 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

XX Disclosure; Page 48; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA;

Query Match 95.3%; Score 345; DB 21; Length 70;  
 Best Local Similarity 95.7%; Pred. No. 1.6e-35;  
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGFQVAGRSARGCGCTSDNDAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60  
 |||||  
 DB 1 TLVWGFQVAGRSARGCGCTSDNDAAEALNASSKEEALQIIREKIPKYLQFHNLSNL 60  
 |||||  
 QY 61 DRIFDKTPEP 70  
 |||||  
 DB 61 DRIFDKTPEP 70  
 |||||

#### RESULT 5

AAAB18692

ID AAB18692 standard; peptide; 70 AA.

XX AAB18692;

XX 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX Synthetic.

OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 66 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

FT Misc-difference 69 /note= "wild type residue replaced with Ala"

Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region

PT XX Disclosure; Page 50; 73pp; English.

PS XX

XX The present sequence represents a mutant peptide, derived from a

CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds

CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded

CC DNA, and interacts with other viral and host proteins. Mutants of the AL1

CC protein are used to produce transgenic plants. The mutation in AL1 is

CC present in a ribosome binding region, and expression of mutant AL1

CC protein imparts increased resistance to geminivirus infection in the

CC plant. Mutant AL1 proteins are useful for producing plants having

CC increased resistance or reduced sensitivity to a geminivirus such as

CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian

CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper

CC virus, cotton leaf curl virus or beet curly top virus.

XX SQ Sequence 70 AA;

Query Match 95.0%; Score 344; DB 21; Length 70;

Best Local Similarity 95.7%; Pred. No. 2.1e-35;

Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

DB 1 TLVWGEFQVAGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70

DB 61 DRIFDKTPEP 70

RESULT 6

AA18684

ID AAB18684 standard; peptide; 70 AA.

XX AAB18684;

AC AAB18684;

XX 22-JAN-2001 (first entry)

DT 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX ribosome binding region; resistance; geminivirus infection.

KW Synthetic.

XX Tomato golden mosaic virus.

OS

XX

XX Key Location/Qualifiers

FH Misc-difference 7 /note= "wild type residue replaced with Ala"

FT Misc-difference 8 /note= "wild type residue replaced with Ala"

FT Misc-difference 9 /note= "wild type residue replaced with Ala"

XX WO200054573-A1.

PN

XX

XX 21-SEP-2000.

PD

XX

XX 15-MAR-2000; 2000WO-US06759.

XX

XX 18-MAR-1999; 99US-0125004.

PR 09-APR-1999; 99US-0289346.

XX (UYN-) UNIV NORTH CAROLINA STATE.

PA Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence

PT encoding a mutant AL1 protein with a mutation in the Rb binding region

PT

XX Claim 52; Page 45; 73pp; English.

PS

XX The present sequence represents a mutant peptide, derived from a

CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds

CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded

CC DNA, and interacts with other viral and host proteins. Mutants of the AL1

CC protein are used to produce transgenic plants. The mutation in AL1 is

CC present in a ribosome binding region, and expression of mutant AL1

CC protein imparts increased resistance to geminivirus infection in the

CC plant. Mutant AL1 proteins are useful for producing plants having

CC increased resistance or reduced sensitivity to a geminivirus such as

CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian

CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper

CC virus, cotton leaf curl virus or beet curly top virus.

XX SQ Sequence 70 AA;

Query Match 94.5%; Score 342; DB 21; Length 70;

Best Local Similarity 95.7%; Pred. No. 3.7e-35;

Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

DB 1 TLVWGEAAVDGRSARGGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70

DB 61 DRIFDKTPEP 70

RESULT 7

AA18690

ID AAB18690 standard; peptide; 70 AA.

XX AAB18690;

AC AAB18690;

XX 22-JAN-2001 (first entry)

DT 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX ribosome binding region; resistance; geminivirus infection.

KW Synthetic.

XX Tomato golden mosaic virus.

OS

XX

XX Key Location/Qualifiers

FH Misc-difference 27 /note= "wild type residue replaced with Ala"

FT Misc-difference 30 /note= "wild type residue replaced with Ala"

XX WO200054573-A1.

PN

XX

XX 21-SEP-2000.

PD

XX

XX 15-MAR-2000; 2000WO-US06759.

XX

XX 18-MAR-1999; 99US-0125004.

PR 09-APR-1999; 99US-0289346.

XX (UYN-) UNIV NORTH CAROLINA STATE.

PA Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

PT

PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 XX  
 XX Disclosure; Page 49; 73pp; English.

CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, bean dwarf mosaic virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA;  
 SQ Query Match 94.5%; Score 342; DB 21; Length 70;  
 Best Local Similarity 95.7%; Pred. No. 3.7e-35;  
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGCTSDNDAALNASSKEALQIIRKIPKYLQFPHNLNSNL 60  
 |||||  
 DB 1 TLVWGEFQVDSARGGCTSDNDAALNASSKEALQIIRKIPKYLQFPHNLNSNL 60  
 |||||

QY 61 DRIFDKTPEP 70  
 |||||  
 DB 61 DRIFDKTPEP 70  
 |||||

RESULT 8  
 AAB18678  
 ID AAB18678 standard; peptide; 70 AA.  
 XX  
 AC AAB18678;  
 DT 22-JAN-2001 (first entry)  
 XX  
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 XX Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 12 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 13 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 15 /note= "wild type residue replaced with Ala"  
 FT Misc-difference 15 /note= "wild type residue replaced with Ala"  
 XX  
 XX WO200054573-A1.  
 FN 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 PA Hanley-Bowdoin L, Orozco BM, Kong L;  
 PI  
 XX

DR WPI; 2000-618851/59.  
 XX Transgenic plants with increased resistance to geminivirus infection  
 PT comprise a nucleic acid construct containing a nucleic acid sequence  
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region  
 PT  
 XX Claim 53; Page 42-43; 73pp; English.

CC The present sequence represents a mutant peptide, derived from a  
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds  
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded  
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1  
 CC protein are used to produce transgenic plants. The mutation in AL1 is  
 CC present in a ribosome binding region, and expression of mutant AL1  
 CC protein imparts increased resistance to geminivirus infection in the  
 CC plant. Mutant AL1 proteins are useful for producing plants having  
 CC increased resistance or reduced sensitivity to a geminivirus such as  
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl  
 CC virus, bean dwarf mosaic virus, African cassava mosaic virus, Indian  
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic  
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper  
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA;  
 SQ Query Match 94.2%; Score 341; DB 21; Length 70;  
 Best Local Similarity 94.3%; Pred. No. 5e-35;  
 Matches 66; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGCTSDNDAALNASSKEALQIIRKIPKYLQFPHNLNSNL 60  
 |||||  
 DB 1 TLVWGEFQVDSARGGCTSDNDAALNASSKEALQIIRKIPKYLQFPHNLNSNL 60  
 |||||

QY 61 DRIFDKTPEP 70  
 |||||  
 DB 61 DRIFDKTPEP 70  
 |||||

RESULT 9  
 AAB18686  
 ID AAB18686 standard; peptide; 70 AA.  
 XX  
 AC AAB18686;  
 DT 22-JAN-2001 (first entry)  
 XX  
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.  
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;  
 KW ribosome binding region; resistance; geminivirus infection.  
 XX  
 XX Synthetic.  
 OS Tomato golden mosaic virus.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 24 /note= "wild type residue replaced with Leu"  
 FT Misc-difference 25 /note= "wild type residue replaced with Leu"  
 FT Misc-difference 26 /note= "wild type residue replaced with Leu"  
 FT Misc-difference 26 /note= "wild type residue replaced with Leu"  
 XX  
 XX WO200054573-A1.  
 FN 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06759.  
 XX  
 XX 18-MAR-1999; 99US-0125004.  
 PR 09-APR-1999; 99US-0289346.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 PA

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XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PS Claim 53; Page 46; 73pp; English.
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 94.2%; Score 341; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 5e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TLVWGEFVAGSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
DB 1 TLVWGEFVAGSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 10
ID AAB18689 standard; peptide; 70 AA.
XX AC AAB18689;
XX DT 22-JAN-2001 (first entry)
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX FH Key Location/Qualifiers
XX FT Misc-difference 22 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX PN WO200054573-A1.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000; 2000WO-US06759.
XX PR 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX XX

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PA XX (UTNC-) UNIV NORTH CAROLINA STATE.
PI XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT Transgenic plants with increased resistance to geminivirus infection
XX PT comprise a nucleic acid construct containing a nucleic acid sequence
XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region
XX PS Disclosure; Page 48-49; 73pp; English.
XX CC The present sequence represents a mutant peptide, derived from a
XX CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX CC protein are used to produce transgenic plants. The mutation in AL1 is
XX CC present in a ribosome binding region, and expression of mutant AL1
XX CC protein imparts increased resistance to geminivirus infection in the
XX CC plant. Mutant AL1 proteins are useful for producing plants having
XX CC increased resistance or reduced sensitivity to a geminivirus such as
XX CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA;
Query Match 93.9%; Score 340; DB 21; Length 70;
Best Local Similarity 95.7%; Pred. No. 6.6e-35;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TLVWGEFVAGSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
DB 1 TLVWGEFVAGSARGGCGTSDNDAALNASSKEALQIIREKIPEKYLFOFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 11
ID AAB18680 standard; peptide; 70 AA.
XX AC AAB18680;
XX DT 22-JAN-2001 (first entry)
XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX KW ribosome binding region; resistance; geminivirus infection.
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX FH Key Location/Qualifiers
XX FT Misc-difference 42 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 43 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 44 /note= "wild type residue replaced with Ala"
XX PN WO200054573-A1.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000; 2000WO-US06759.
XX XX

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PN WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 52; Page 44; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, bean dwarf mosaic virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 92.5%; Score 335; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 2.8e-34;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TLVWGEFQVAGRSARGGCGTNDAAALNASSKEEALQIREKIPKYLQFHNLSNL 60
DB 1 TLVWGEFQVAGRSARGGCGTNDAAALNASSKEEALQIREKIPKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 DRIFDKTPEP 70
RESULT 14
AAB18683
XX ID AAB18683 standard; peptide; 70 AA.
XX AC AAB18683;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX Key Location/Qualifiers
XX Misc-difference 59 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 61 /note= "wild type residue replaced with Ala"
XX FT

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FT Misc-difference 62 /note= "wild type residue replaced with Ala"
XX WO200054573-A1.
XX 21-SEP-2000.
XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX Claim 53; Page 45; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, bean dwarf mosaic virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
Query Match 92.3%; Score 334; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 3.8e-34;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TLVWGEFQVAGRSARGGCGTNDAAALNASSKEEALQIREKIPKYLQFHNLSNL 60
DB 1 TLVWGEFQVAGRSARGGCGTNDAAALNASSKEEALQIREKIPKYLQFHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 61 AAFDKTPEP 70
RESULT 15
AAB18682
XX ID AAB18682 standard; peptide; 70 AA.
XX AC AAB18682;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX Key Location/Qualifiers
XX Misc-difference 52
XX FT

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FT Misc-difference 54 /note= "wild type residue replaced with Ala"  
 FT FT Misc-difference 55 /note= "wild type residue replaced with Ala"  
 FT FT Misc-difference 55 /note= "wild type residue replaced with Ala"

XX WO200054573-A1.

PN 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UYN-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence

PT encoding a mutant Al1 protein with a mutation in the Rb binding region

PT

XX Claim 53; Page 44-45; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a

XX geminivirus replication (Rep) protein, also known as Al1. Al1 binds

XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded

XX DNA, and interacts with other viral and host proteins. Mutants of the Al1

XX protein are used to produce transgenic plants. The mutation in Al1 is

XX present in a ribosome binding region, and expression of mutant Al1

XX plant imparts increased resistance to geminivirus infection in the

XX plant. Mutant Al1 proteins are useful for producing plants having

XX increased resistance or reduced sensitivity to a geminivirus such as

XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian

XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper

XX virus, cotton leaf curl virus or beet curly top virus.

XX SQ Sequence 70 AA;

Query Match 91.7%; Score 332; DB 21; Length 70;

Best Local Similarity 94.3%; Pred. NO. 6.7e-34;

Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRGCGCQTNDAAAEALNASSKEALQIIRKIPKYLFOFHNLNSNL 60

Db 1 TLVWGEFQVAGRGCGCQTNDAAAEALNASSKEALQIIRKIPKYLFOFHNLNSNL 60

QY 61 DRIFDKTPEP 70

Db 61 DRIFDKTPEP 70

Search completed: December 23, 2003, 08:56:31

Job time : 32.6667 secs





Db 110 TIEMGFQVDSRGSGQSSANDSYAKALNADSIESTILKEEQKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70  
:|||||

Db 170 ERIFVKVPEP 179

RESULT 2  
US-08-838-151A-46  
; Sequence 46, Application US/08838151A  
; Patent No. 6291743  
; GENERAL INFORMATION:  
; APPLICANT: Stout, John T  
; APPLICANT: Luu, Hang T  
; APPLICANT: Maxwell, Douglas  
; APPLICANT: Ahlquist, Paul  
; APPLICANT: Hanson, Steve  
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
; STREET: Two Prudential Plaza, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838.151A  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mueller, Lisa V  
; REGISTRATION NUMBER: 38,978  
; REFERENCE/DOCKET NUMBER: SVS3801P0260  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-616-5400  
; TELEFAX: 312-616-5400  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 353 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-838-151A-46

Query Match 61.3%; Score 222; DB 3; Length 353;  
Best Local Similarity 60.0%; Pred. No. 1.7e-20;  
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGFEFVAGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLFPQPHNLNSNL 60  
:|||||

Db 110 TIEMGFQVDSRGSGQSSANDSYAKALNADSIESTILKEEQKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70  
:|||||

Db 170 ERIFVKVPEP 179

RESULT 3  
US-08-838-151A-49  
; Sequence 49, Application US/08838151A  
; Patent No. 6291743  
; GENERAL INFORMATION:  
; APPLICANT: Stout, John T  
; APPLICANT: Luu, Hang T  
; APPLICANT: Maxwell, Douglas  
; APPLICANT: Ahlquist, Paul

; APPLICANT: Hanson, Steve  
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
; STREET: Two Prudential Plaza, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838.151A  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mueller, Lisa V  
; REGISTRATION NUMBER: 38,978  
; REFERENCE/DOCKET NUMBER: SVS3801P0260  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-616-5400  
; TELEFAX: 312-616-5400  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 353 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-838-151A-49

Query Match 61.3%; Score 222; DB 3; Length 353;  
Best Local Similarity 60.0%; Pred. No. 1.7e-20;  
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGFEFVAGRSARGGCGTSDNDAAEALNASSKEEALQIIREKIPKYLFPQPHNLNSNL 60  
:|||||

Db 110 TIEMGFQVDSRGSGQSSANDSYAKALNADSIESTILKEEQKDYVLQHHNIRSNL 169

QY 61 DRIFDKTPEP 70  
:|||||

Db 170 ERIFVKVPEP 179

RESULT 4  
US-08-838-151A-52  
; Sequence 52, Application US/08838151A  
; Patent No. 6291743  
; GENERAL INFORMATION:  
; APPLICANT: Stout, John T  
; APPLICANT: Luu, Hang T  
; APPLICANT: Maxwell, Douglas  
; APPLICANT: Ahlquist, Paul  
; APPLICANT: Hanson, Steve  
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz  
; STREET: Two Prudential Plaza, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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i MOLECULE TYPE: protein
US-08-838-151A-55

Query Match          61.3%; Score 222; DB 3; Length 353;
Best Local Similarity 60.0%; Pred. No. 1.7e-20;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY      1 TLVWGEPQAGRSARGCOTSNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSLD 60
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB     110 TLMGGFQDGRSARCGQSANDSYAKALNADSIESALTILKEEQKYVLQHINIRSNL 169
               :|||||
QY      61 DRIFDKTPEP 70
       :|||||
DB     170 ERIPVKVEP 179
               :|||||

RESULT 6
US-08-809-103B-2
; Sequence 2, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEX: (703) 685-0573
; FAX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-2

Query Match          61.3%; Score 222; DB 3; Length 359;
Best Local Similarity 58.0%; Pred. No. 1.7e-20;
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY      2 LVWGEQVAGRSARGCOTSNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSLD 61
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB     111 LMGTFQIDGRSARCGQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFHNINSND 170
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Db 171 KVFQVPPAP 179

# RESULT 7

US-08-809-103B-4  
 ; Sequence 4, Application US/08809103B  
 ; Patent No. 6133505  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GRONENBORN, Bruno  
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: YOUNG & THOMPSON  
 ; STREET: 745 South 23rd Street  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; COUNTRY: U.S.A.  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/809,103B  
 ; FILING DATE: 17-MAR-1997  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: FR 94.11040  
 ; FILING DATE: 15-SEP-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/FR95/01192  
 ; FILING DATE: 15-SEP-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: PATCH, Andrew J.  
 ; REGISTRATION NUMBER: 32,925  
 ; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 521-2297  
 ; TELEFAX: (703) 685-0573  
 ; TELEX: 248425 EMBON  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 359 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-809-103B-4

Query Match 61.3%; Score 222; DB 3; Length 359;

Best Local Similarity 58.0%; Pred. No. 1.7e-20;  
 Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 LVWGFQVAGRGCGCOTSDNDAAEALNASSKEALQIREKIPKYLQFPHNLSNLD 61  
 Db 111 LEMGTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLFHFNINSNLD 170  
 QY 62 RIFDKTPEP 70  
 Db 171 KVFQVPPAP 179

# RESULT 8

US-08-809-103B-6  
 ; Sequence 6, Application US/08809103B  
 ; Patent No. 6133505  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GRONENBORN, Bruno  
 ; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: YOUNG & THOMPSON  
 STREET: 745 South 23rd Street  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/809,103B  
 FILING DATE: 17-MAR-1997  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 94.11040  
 FILING DATE: 15-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/FR95/01192  
 FILING DATE: 15-SEP-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PATCH, Andrew J.  
 REGISTRATION NUMBER: 32,925  
 REFERENCE/DOCKET NUMBER: USB94AL CNR TOM  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 521-2297  
 TELEFAX: (703) 685-0573  
 TELEX: 248425 EMBON  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 359 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-809-103B-6

Query Match 61.3%; Score 222; DB 3; Length 359;

Best Local Similarity 58.0%; Pred. No. 1.7e-20;  
 Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 LVWGFQVAGRGCGCOTSDNDAAEALNASSKEALQIREKIPKYLQFPHNLSNLD 61  
 Db 111 LEMGTQIDGRSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLFHFNINSNLD 170  
 QY 62 RIFDKTPEP 70  
 Db 171 KVFQVPPAP 179

# RESULT 9

US-08-809-103B-8  
 ; Sequence 8, Application US/08809103B  
 ; Patent No. 6133505  
 ; GENERAL INFORMATION:

APPLICANT: GRONENBORN, Bruno  
 TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT  
 TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: YOUNG & THOMPSON  
 STREET: 745 South 23rd Street  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/809,103B

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; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8

Query Match 61.3%; Score 222; DB 3; Length 359;
Best Local Similarity 58.0%; Pred. No. 1.7e-20;
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 LVNGEFQVAGRSARGGCGTSDNDAAEALNASSKEEALQIIRKIPKYLQFHNLSNLD 61
Db 111 LEWTFDIDGRSARGGCGTNDAYAKAINAGSKQALDVIKELAPRDYVLHFNINSNLD 170

QY 62 RIFDKTPEP 70
Db 171 KVFOVPPAP 179

RESULT 10
US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match 60.8%; Score 220; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 3.1e-20;
Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVNGEFQVAGRSARGGCGTSDNDAAEALNASSKEEALQIIRKIPKYLQFHNLSNLD 60
Db 110 TIWGFDFIDGRSARGGCGQSANDSYAKALNASSVQSALAVLRBEQPKDFVLQNHINRSNLD 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-2

Query Match 60.8%; Score 220; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 3.1e-20;
Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVNGEFQVAGRSARGGCGTSDNDAAEALNASSKEEALQIIRKIPKYLQFHNLSNLD 60
Db 110 TIWGFDFIDGRSARGGCGQSANDSYAKALNASSVQSALAVLRBEQPKDFVLQNHINRSNLD 169

QY 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 11
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-4

Query Match 60.8%; Score 220; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 3.1e-20;
Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 TLVNGEFQVAGRSARGGCGTSDNDAAEALNASSKEEALQIIRKIPKYLQFHNLSNLD 60
Db 110 TIWGFDFIDGRSARGGCGQSANDSYAKALNASSVQSALAVLRBEQPKDFVLQNHINRSNLD 169
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QY      61 DRIFDKTPEP 70
DB      170 ERIFAKAPEP 179

RESULT 12
US-08-838-151A-6
; Sequence 6, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-6

Query Match      60.8%; Score 220; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 3.1e-20;
Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY      1 TLVWGEFQVAGRSARGCGTSDNDAARALNASSKEALQIIREKIPEKYLQFPHNLNSNL 60
DB      110 TIEWGDFQIDGRSARGCGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNRNSNL 169

QY      61 DRIFDKTPEP 70
DB      170 ERIFAKAPEP 179

RESULT 13
US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8

Query Match      60.8%; Score 220; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 3.1e-20;
Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY      1 TLVWGEFQVAGRSARGCGTSDNDAARALNASSKEALQIIREKIPEKYLQFPHNLNSNL 60
DB      110 TIEWGDFQIDGRSARGCGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNRNSNL 169

QY      61 DRIFDKTPEP 70
DB      170 ERIFAKAPEP 179

RESULT 14
US-08-838-151A-24
; Sequence 24, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8

Query Match      60.8%; Score 220; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 3.1e-20;
Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY      1 TLVWGEFQVAGRSARGCGTSDNDAARALNASSKEALQIIREKIPEKYLQFPHNLNSNL 60
DB      110 TIEWGDFQIDGRSARGCGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNRNSNL 169

QY      61 DRIFDKTPEP 70
DB      170 ERIFAKAPEP 179

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; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8

Query Match      60.8%; Score 220; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 3.1e-20;
Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY      1 TLVWGEFQVAGRSARGCGTSDNDAARALNASSKEALQIIREKIPEKYLQFPHNLNSNL 60
DB      110 TIEWGDFQIDGRSARGCGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNRNSNL 169

QY      61 DRIFDKTPEP 70
DB      170 ERIFAKAPEP 179

RESULT 14
US-08-838-151A-24
; Sequence 24, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-8

Query Match      60.8%; Score 220; DB 3; Length 361;
Best Local Similarity 57.1%; Pred. No. 3.1e-20;
Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY      1 TLVWGEFQVAGRSARGCGTSDNDAARALNASSKEALQIIREKIPEKYLQFPHNLNSNL 60
DB      110 TIEWGDFQIDGRSARGCGQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNRNSNL 169

QY      61 DRIFDKTPEP 70
DB      170 ERIFAKAPEP 179

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; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-24

Query Match          57.2%; Score 207; DB 3; Length 357;
Best Local Similarity 65.6%; Pred.No. 1.5e-18;
Matches 40; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY      4 WGEFQVAGRSARGGCGQTSNDAAAEALNASKEEALQIIREKIPKYLQFQFHNLSNLDRI 63
Db      111 FGVSDIGRSARGGQGSANDAVAEALNSGSKSEALNLIKKEAPKDYILQFHNLSNLDRI 170

QY      64 F 64
Db      171 F 171

Search completed: December 23, 2003, 08:59:35
Job time : 11.6667 secs

;
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-27

Query Match          57.2%; Score 207; DB 3; Length 357;
Best Local Similarity 65.6%; Pred.No. 1.5e-18;
Matches 40; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY      4 WGEFQVAGRSARGGCGQTSNDAAAEALNASKEEALQIIREKIPKYLQFQFHNLSNLDRI 63
Db      111 FGVSDIGRSARGGQGSANDAVAEALNSGSKSEALNLIKKEAPKDYILQFHNLSNLDRI 170

QY      64 F 64
Db      171 F 171

RESULT 15
US-08-838-151A-27
; Sequence 27, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Anquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-27
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3	356	98.3	70	10	US-09-289-346A-11	Sequence 11, Appl
4	345	95.3	70	10	US-09-289-346A-12	Sequence 12, Appl
5	344	95.0	70	10	US-09-289-346A-16	Sequence 16, Appl
6	342	94.5	70	10	US-09-289-346A-8	Sequence 8, Appl
7	342	94.5	70	10	US-09-289-346A-14	Sequence 14, Appl
8	341	94.2	70	10	US-09-289-346A-2	Sequence 2, Appl
9	341	94.2	70	10	US-09-289-346A-10	Sequence 10, Appl
10	340	93.9	70	10	US-09-289-346A-13	Sequence 13, Appl
11	338	93.4	70	10	US-09-289-346A-4	Sequence 4, Appl
12	338	93.4	70	10	US-09-289-346A-15	Sequence 15, Appl
13	335	92.5	70	10	US-09-289-346A-5	Sequence 5, Appl
14	334	92.3	70	10	US-09-289-346A-7	Sequence 7, Appl
15	332	91.7	70	10	US-09-289-346A-6	Sequence 6, Appl

QY 61 DRIEKTPEP 70

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61 DRIEDKTEP 70

Db 61 DRIFDKTPEP 70  
|||||  
110 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 169

RESULT 2  
US-09-289-346A-1  
; Sequence 1, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
US-09-289-346A-1

Query Match 98.3%; Score 356; DB 10; Length 70;  
Best Local Similarity 98.6%; Pred. No. 4.8e-38;  
Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60  
Db 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60

QY 61 DRIFDKTPEP 70  
Db 61 DRIFDKTPEP 70  
|||||

RESULT 3  
US-09-289-346A-11  
; Sequence 11, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 356  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (354)  
; OTHER INFORMATION: Unsure about sequence assignment  
US-09-289-346A-11

Query Match 98.3%; Score 356; DB 10; Length 356;  
Best Local Similarity 98.6%; Pred. No. 4e-37;  
Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60  
Db 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60  
|||||

Db 110 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 169

QY 61 DRIFDKTPEP 70  
Db 170 DRIFDKTPEP 179  
|||||

RESULT 4  
US-09-289-346A-12  
; Sequence 12, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
US-09-289-346A-12

Query Match 95.3%; Score 345; DB 10; Length 70;  
Best Local Similarity 95.7%; Pred. No. 1.2e-36;  
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60  
Db 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60  
|||||

QY 61 DRIFDKTPEP 70  
Db 61 DRIFDKTPEP 70  
|||||

RESULT 5  
US-09-289-346A-16  
; Sequence 16, Application US/09289346A  
; Patent No. US20020138867A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanley-Bowdoin, Linda  
; APPLICANT: Orozco, Beverly M.  
; APPLICANT: Kong, Ling-Jie  
; APPLICANT: Gruissem, Wilhelm  
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS  
; FILE REFERENCE: Hanley-Bowdoin et al.  
; CURRENT APPLICATION NUMBER: US/09/289,346A  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Tomato golden mosaic virus  
US-09-289-346A-16

Query Match 95.0%; Score 344; DB 10; Length 70;  
Best Local Similarity 95.7%; Pred. No. 1.7e-36;  
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60  
Db 1 TLVWGEFQVAGSARGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLQFHNLSNL 60  
|||||



```

QY      61 DRIFDKTPEP 70
Db      61 DRIFDATPAP 70

RESULT 6
US-09-289-346A-8
; Sequence 8, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)..(8)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (FQ118->M118).
US-09-289-346A-8

Query Match      94.5%; Score 342; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 3e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TLVWGEFOVAGRSARGGCOTSDNDAALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db      1 TLVWGEAIVDGRSARGGCOTSDNDAALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

RESULT 7
US-09-289-346A-14
; Sequence 14, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-14

Query Match      94.5%; Score 342; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 3e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

RESULT 8
US-09-289-346A-2
; Sequence 2, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (12)..(15)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of TGMV Rep
; OTHER INFORMATION: Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacement (RSAR125->AAAA125).
US-09-289-346A-2

Query Match      94.2%; Score 341; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 4e-36;
Matches 66; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 TLVWGEFOVAGRSARGGCOTSDNDAALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
Db      1 TLVWGEFQVDAAGAGGCOTSDNDAALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

RESULT 9
US-09-289-346A-10
; Sequence 10, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-10

Query Match      94.5%; Score 342; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 3e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      61 DRIFDKTPEP 70
Db      61 DRIFDKTPEP 70

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Tue Dec 23 09:55:39 2003

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; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)...(26)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with leucine
; OTHER INFORMATION: replacements (AAAL136->LLLL136).
US-09-289-346A-10

Query Match          94.2%; Score 341; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 4e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGCGCOTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
   |||||
DB 1 TLVWGEFQVAGRSARGCGCOTSDNDLLEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
   |||||
DB 61 DRIFDKTPEP 70

RESULT 10
US-09-289-346A-13
; Sequence 13, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-13

Query Match          93.9%; Score 340; DB 10; Length 70;
Best Local Similarity 95.7%; Pred. No. 5.4e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGCGCOTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
   |||||
DB 1 TLVWGEFQVAGRSARGCGCOTSDNAAAALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
   |||||
DB 61 DRIFDKTPEP 70

RESULT 11
US-09-289-346A-4
; Sequence 4, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
```

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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (42)...(44)
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: TGMV Rep Protein (aa 110-179) with alanine
; OTHER INFORMATION: replacements (REK154->AAA154).
US-09-289-346A-4

Query Match          93.4%; Score 338; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 9.7e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGCGCOTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
   |||||
DB 1 TLVWGEFQVAGRSARGCGCOTSDNAAAALNASSKEEALQIIRKIPKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
   |||||
DB 61 DRIFDKTPEP 70

RESULT 12
US-09-289-346A-15
; Sequence 15, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: Hanley-Bowdoin et al.
; CURRENT APPLICATION NUMBER: US/09/289,346A
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-09-289-346A-15

Query Match          93.4%; Score 338; DB 10; Length 70;
Best Local Similarity 94.3%; Pred. No. 9.7e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGCGCOTSDNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
   |||||
DB 1 TLVWGEFQVAGRSARGCGCOTSDNAAAALNASSAAAAAQIIRKIPKYLFOFHNLSNL 60

QY 61 DRIFDKTPEP 70
   |||||
DB 61 DRIFDKTPEP 70

RESULT 13
US-09-289-346A-5
; Sequence 5, Application US/09289346A
; Patent No. US20020138867A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Kong, Ling-Jie
; APPLICANT: Gruissem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 10 Seconds  
(without alignments)  
673.181 Million cell updates/sec

Title: US-09-289-346B-9

Perfect score: 362

Sequence: 1 TLVWGSEFQVAGRSARGCQT.....FQFHNLSNMLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	356	98.3	352	1 QOCVLI	Al1 protein - toma
2	256	70.7	361	1 QOCVPT	Al1 protein - toma
3	243	67.1	358	2 S07S94	hypothetical prote
4	236	65.2	362	1 JQ1887	Al1 protein - toma
5	229	63.3	359	2 S39211	gene C1 protein -
6	225	62.2	349	2 JQ2300	replicase - pepp
7	225	62.2	349	2 S31875	Al1 protein - pepp
8	222	61.3	359	2 S22593	hypothetical prote
9	219	60.5	351	2 JQ2327	Al1 protein - Indi
10	219	60.5	355	1 QOCVW1	AV1 protein - abut
11	216	59.7	358	1 JQ1870	Al1 protein - toma
12	216	59.7	359	2 S39235	gene C1 protein -
13	216	59.7	385	2 S28360	Al1 protein - beet
14	209	57.7	360	2 S59885	replication-associ
15	207	57.2	357	1 QOCVC1	Al1 protein - toma
16	142	39.2	131	2 S45059	AC1 protein (clone
17	125	34.5	347	1 QOCV81	Al1 protein - squa
18	68	18.8	587	2 JQ1439	Pc gamma (IgG) rec
19	67	18.5	840	2 T36175	probable large ATP
20	64.5	17.8	299	2 B71967	probable peptidyl-
21	63.5	17.5	642	2 D90558	topoisomerase iv s
22	63	17.4	714	2 C95382	probable ferrichro
23	62.5	17.3	447	2 T12544	hypothetical prote
24	62	17.1	154	2 AD3475	protein-Npi-phosph
25	62	17.1	181	2 G37976	conserved hypochet
26	62	17.1	295	2 D42452	C1 protein - tobac
27	62	17.1	340	2 B97011	probably O-sialogl
28	61.5	17.0	201	2 A81380	probable flagellar
29	61.5	17.0	481	2 A70091	probable phosphoes

30 61 16.9 1502 1 RGVH11  
31 50.5 16.7 1713 2 AS5347  
32 60.5 16.7 2137 2 T05244  
33 60 16.6 160 2 G82060  
34 60 16.6 319 2 B90067  
35 60 16.6 447 2 S52437  
36 60 16.6 988 2 P86316  
37 59.5 16.4 1033 2 E97700  
38 59 16.3 338 2 AG3582  
39 59 16.3 337 2 B71078  
40 59 16.3 416 2 A82892  
41 59 16.3 862 2 H82182  
42 59 16.3 1287 2 S55954  
43 59 16.3 1341 2 JG0166  
44 58.5 16.2 180 2 D84082  
45 58.5 16.2 230 2 S46332

## ALIGNMENTS

### RESULT 1

QOCVLI

Al1 protein - tomato golden mosaic virus

C:Species: tomato golden mosaic virus

A:Note: Host Nicotiana sp. (tobacco)

C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Apr-1994

C:Accession: A04170

R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.

EMBO J. 3, 2197-2205, 1984

A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomat

A:Reference number: A04163

A:Accession: A04170

A:Molecule type: DNA

A:Residues: 1-352 <HAM>

C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A

C:Genetics:

A:Map position: segment A

C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 98.3%; Score 356; DB 1; Length 352;  
Best Local Similarity 98.6%; Pred. No. 1.7e-32;  
Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLVWGSEFQVAGRSARGCQTSDNAAEALNASSKEKALQIIREKIPKYLQFHNLSNL 60

DB 111 TLVWGSEFQVAGRSARGCQTSDNAAEALNASSKEKALQIIREKIPKYLQFHNLSNL 170

QY 61 DRIFDKTPEP 70

DB 171 DRIFDKTPEP 180

### RESULT 2

QOCVPT

Al1 protein - potato yellow mosaic virus (isolate Venezuela)

C:Species: potato yellow mosaic virus

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jun-2000

C:Accession: J00364

R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.

J. Gen. Virol. 72, 1515-1520, 1991

A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yel

A:Reference number: J00362; MUID:91311403; PMID:1856690

A:Accession: J00364

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-361 <COU>

A:Cross-references: GB:D00940; NID:G222458; PIDN:BAA00782.1; PID:G222459

C:Genetics:

A:Map position: segment A

C:Superfamily: tomato golden mosaic virus Al1 protein



A;Accession: S31875

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-349 <TOR>

A;Cross-references: EMBL:X70418; NID:G61023; PIDN:CAA49856.1; PID:G61025

A;Note: the source is designated as pepper huasteco virus

C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 62.2%; Score 225; DB 2; Length 349;

Best Local Similarity 60.0%; Pred. No. 1.1e-17; Indels 0; Gaps 0;

Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLVWGFQVAGRSARGCGCQTSNDAAAEALNASSKEALQIIRKIPKYLFOFHNLSNLD 60

Db 110 TVEWGFQIDGRSARGCGQTSNDAYAKALNSAEALQIIRKIPKYLFOFHNLSNLD 169

Qy 61 DRFDKTPPEP 70

Db 170 NRIFQTPPEP 179

RESULT 8

S22593

hypothetical protein C4 - tomato yellow leaf curl virus

C;Species: tomato yellow leaf curl virus

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Sep-1999

C;Accession: S22593

R;Kheyr-Pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.

Nucleic Acids Res. 19, 6763-6769, 1991

A;Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite

A;Reference number: S22588; MUID:92107660; PMID:1840676

A;Accession: S22593

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-359 <RHE>

A;Cross-references: EMBL:X61153; NID:G62211; PIDN:CAA43466.1; PID:G62217

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991

C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 61.3%; Score 222; DB 2; Length 359;

Best Local Similarity 58.0%; Pred. No. 2.4e-17; Indels 0; Gaps 0;

Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 2 LVWGFQVAGRSARGCGCQTSNDAAAEALNASSKEALQIIRKIPKYLFOFHNLSNLD 61

Db 111 LEWGFQIDGRSARGCGQTSNDAYAKALNSAEALQIIRKIPKYLFOFHNLSNLD 170

Qy 62 RFDKTPPEP 70

Db 171 KVFQVPPAP 179

RESULT 9

QJ0327

AL1 protein - Indian caseava mosaic virus

A;Alternate names: replication-associated protein

C;Species: Indian caseava mosaic virus

C;Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 20-Sep-1999

C;Accession: JQ2327; S35883

R;Hong, Y.G.; Robinson, D.J.; Harrison, B.D.

J. Gen. Virol. 74, 2437-2443, 1993

A;Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-trans

A;Reference number: JQ2326; MUID:94065670; PMID:8245859

A;Accession: JQ2327

A;Molecule type: DNA

A;Residues: 1-351 <HON>

A;Cross-references: EMBL:Z24758; NID:G395351; PIDN:CAA80891.1; PID:G584046

C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match

Best Local Similarity 60.5%; Score 219; DB 2; Length 351;

Matches 42; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 4 WGEFQVAGRSARGCGCQTSNDAAAEALNASSKEALQIIRKIPKYLFOFHNLSNLDRI 63

Db 113 MGTQIDGRSARGCGQTSANDAYAAALNSGSKSEALQIIRKIPKYLFOFHNLSNLDRI 172

Qy 64 FDKTPPEP 70

Db 173 FTKPPPP 179

RESULT 10

QJ0327

AV1 protein - abutilon mosaic virus (isolate West India)

C;Species: abutilon mosaic virus

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 08-Apr-1994

C;Accession: A36214

R;Frischmuth, T.; Zimmatt, G.; Jeske, H.

Virol. 178, 461-468, 1990

A;Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as w

A;Reference number: A36214; MUID:91020984; PMID:2219703

A;Accession: A36214

A;Molecule type: DNA

A;Residues: 1-355 <FRI>

A;Cross-references: EMBL:X15983

C;Genetics:

A;Map position: segment A

C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match 60.5%; Score 219; DB 1; Length 355;

Best Local Similarity 58.6%; Pred. No. 5.2e-17;

Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TLVWGFQVAGRSARGCGCQTSNDAAAEALNASSKEALQIIRKIPKYLFOFHNLSNLD 60

Db 110 TAEWGFQIDGRSARGCGQTSANDAYAKALNSAEALQIIRKIPKYLFOFHNLSNLD 169

Qy 61 DRFDKTPPEP 70

Db 170 ERIFAKAPEP 179

RESULT 11

QJ01870

AL1 protein - tomato mottle virus (isolate Florida)

C;Species: tomato mottle virus

C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 07-May-1999

C;Accession: JQ1870

R;Abouzid, A.M.; Polston, J.E.; Hiebert, E.

J. Gen. Virol. 73, 3225-3229, 1992

A;Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated fr

A;Reference number: JQ1869; MUID:93107858; PMID:1469361

A;Accession: JQ1870

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-358 <ABO>

A;Cross-references: GB:L14460

C;Genetics:

A;Map position: segment A

C;Superfamily: tomato golden mosaic virus AL1 protein

Query Match

Best Local Similarity 59.7%; Score 216; DB 1; Length 358;

Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLVWGFQVAGRSARGCGCQTSNDAAAEALNASSKEALQIIRKIPKYLFOFHNLSNLD 60

Db 107 TIWGFQIDGRSARGCGQTSANDAYAKALNSAEALQIIRKIPKYLFOFHNLSNLD 166

Qy 61 DRFDKTPPEP 70

Db 167 ERIFAKAPEP 176

RESULT 12

S39235

Gene C1 protein - tomato yellow leaf curl virus  
 C:Species: tomato yellow leaf curl virus  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Sep-1997  
 C:Accession: S39235  
 R:Crepi, S.; Norris, E.; Vaira, A.; Bosco, D.; Accotto, G.  
 submitted to the EMBL Data Library, December 1993  
 A:Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.  
 A:Reference number: S39233  
 A:Accession: S39235  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-359 <CR>  
 A:Cross-references: EMBL:Z28390; NID:G1041671; PID:G1334964  
 C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.7%; Score 216; DB 2; Length 359;  
 Best Local Similarity 56.5%; Pred. No. 1.2e-16;  
 Matches 39; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 2 LWGEFQVAGRSARGGCGTSDNDAAEALNASSKEALQIREKIPEKYLQFHNLSNLD 61

DB 111 LEWTFQIDGRSARGGQQTANDAYAKALNARKSEALDVIKLAPRDYVLHFNHNSNLD 170

QY 62 RIFDKTPPEP 70

DB 171 KVQVPPAP 179

RESULT 13

S28360  
 AL1 protein - beet curly top virus  
 C:Species: beet curly top virus  
 C:Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Sep-1999  
 C:Accession: S28360  
 R:Stanley, J.; Markham, P.G.; Callis, R.J.; Pinner, M.S.  
 EMBL J. 5, 1761-1767, 1986  
 A:Title: The nucleotide sequence of an infectious clone of the geminivirus beet curly top virus  
 A:Reference number: S28360  
 A:Accession: S28360  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-385 <STA>  
 A:Cross-references: GB:M24597; EMBL:X04144; NID:G210678; PIDN:AAA42751.1; PID:G210679  
 C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.7%; Score 216; DB 2; Length 385;  
 Best Local Similarity 55.7%; Pred. No. 1.3e-16;  
 Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGCGTSDNDAAEALNASSKEALQIREKIPEKYLQFHNLSNLD 60

DB 137 TIWGEFQIDGRSARGGQQTANDSYAKALNATSLDQALQIIEKPEQPKDYFLQHNLLNNA 196

QY 61 DRIFDKTPPEP 70

DB 197 QKIFORPPDP 206

RESULT 14

S59885  
 replication-associated protein C1 - tomato yellow leaf curl virus  
 C:Species: tomato yellow leaf curl virus  
 C:Date: 14-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 20-Sep-1999  
 C:Accession: S59885  
 R:Hong, Y.; Harrison, B.D.  
 submitted to the EMBL Data Library, February 1995  
 A:Description: Nucleotide sequences from tomato leaf curl viruses from different countries  
 A:Reference number: S58346  
 A:Accession: S59885  
 A:Status: preliminary  
 A:Molecule type: DNA

A:Residues: 1-360 &lt;HON&gt;

A:Cross-references: EMBL:Z48182; NID:G944838; PIDN:CAA88229.1; PID:G974211

C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 57.7%; Score 209; DB 2; Length 360;

Best Local Similarity 60.6%; Pred. No. 7.2e-16;

Matches 40; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 4 WGEFQVAGRSARGGCGTSDNDAAEALNASSKEALQIREKIPEKYLQFHNLSNLDRI 63

DB 113 FGVSQIDGRSARGGQQTANDAYAEALNSGKAALDILREKAPKDFVLQFHNLSNLDRI 172

QY 64 FDKTPEP 69

DB 173 FTPSAE 178

RESULT 15

QOCVCI  
 AL1 protein - tomato yellow leaf curl virus  
 N:Alternate names: C1 protein  
 C:Species: tomato yellow leaf curl virus  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
 C:Accession: D40779  
 R:Navot, N.; Pichersky, B.; Zeidan, M.; Zamir, D.; Czosnek, H.  
 Virology 185, 151-161, 1991  
 A:Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single ORF  
 A:Reference number: A40779; MUID:92024070; PMID:1926771  
 A:Accession: D40779  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-357 <NAV>  
 A:Cross-references: GB:X15656; NID:G62204; PIDN:CAA33688.1; PID:G62207  
 C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 57.2%; Score 207; DB 1; Length 357;

Best Local Similarity 65.6%; Pred. No. 1.2e-15;

Matches 40; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 4 WGEFQVAGRSARGGCGTSDNDAAEALNASSKEALQIREKIPEKYLQFHNLSNLDRI 63

DB 111 FGVSQIDGRSARGGQQTANDAYAEALNSGKAALDILREKAPKDFVLQFHNLSNLDRI 170

QY 64 F 64

DB 171 F 171

Search completed: December 23, 2003, 09:05:24

Job time : 11 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:51:23 ; Search time 5.77778 Seconds  
(without alignments)  
569.747 Million cell updates/sec

Title: US-09-289-346B-9

Perfect score: 362

Sequence: 1 TLVWGFQVAGRSARGCQT.....FOFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	356	98.3	352	1 VAL1_TGMV	P03567 tomato gold
2	256	70.7	361	1 VAL1_PYMV	P27258 potato yell
3	243	67.1	358	1 VAL1_CLVK	P14982 cassava lat
4	243	67.1	358	1 VAL1_CLVN	P14972 cassava lat
5	236	65.2	362	1 VAL1_TYLC	P36279 tomato yell
6	229	63.3	359	1 VAL1_TYLCU	P38609 tomato yell
7	225	62.2	349	1 VAL1_PHVU	Q06923 pepper husk
8	222	61.3	359	1 VAL1_TYLCM	P27260 tomato yell
9	220	60.8	353	1 VAL1_BGMV	P05175 bean golden
10	219	60.5	355	1 VAL1_ABMVW	P21947 abutilon mo
11	216	59.7	358	1 VAL1_BCTV	P14991 beet curly
12	216	59.7	361	1 VAL1_TMOV	Q06657 tomato molt
13	207	57.2	357	1 VAL1_TYLCV	P27359 tomato yell
14	125	34.5	347	1 VAL1_SLVC	P29048 squash leaf
15	65.5	18.1	298	1 OUG2_CHICK	Q90XB3 gallus gall
16	64.5	17.8	299	1 Y175_HELPJ	Q9ZMG7 helicobacte
17	62.5	17.3	447	1 TEL2_HUMAN	Q9Y4P3 homo sapien
18	62	17.1	295	1 VAL1_TYDVA	P31617 tobacco vel
19	61	16.9	1502	1 CVPL_YEAST	P12351 saccharomyc
20	60.5	16.7	259	1 FLGH_VIRVU	Q8dfj1 vibrio vuln
21	60.5	16.7	1713	1 LMA3_HUMAN	Q16787 homo sapien
22	60	16.6	319	1 LDH2_STAAW	Q9FR35 staphylococ
23	60	16.6	319	1 LDH2_STAAW	Q8NUM9 staphylococ
24	60	16.6	447	1 CDSA_DROME	P56079 d phosphati
25	60	16.6	719	1 CAT3_NEUCR	Q9c169 neurospora
26	59.5	16.4	476	1 DGRE_HUMAN	Q96df8 homo sapien
27	59.5	16.4	479	1 DGRE_MOUSE	Q70279 mus musculu
28	59	16.3	1287	1 SKI2_YEAST	P35207 saccharomyc
29	58.5	16.2	297	1 RPP_PABVP	P06747 rabies viru
30	58.5	16.2	299	1 Y175_HELPY	P56112 helicobacte
31	58.5	16.2	367	1 LHX4_MOUSE	P53776 mus musculu
32	58.5	16.2	491	1 AMPA_ANASP	Q82064 anabaena sp
33	58.5	16.2	589	1 YB67_HABIN	P45221 haemophilus

34 58.5 16.2 1044 1 RUB1\_SCHPO  
35 58 16.0 207 1 IL6\_MARMO  
36 58 16.0 256 1 UT11\_YEAST  
37 58 16.0 617 1 YACH\_ECOLI  
38 58 16.0 874 1 SLAP\_BACIL  
39 57.5 15.9 136 1 Y452\_CABEL  
40 57 15.7 355 1 CRTB\_RHOSH  
41 57 15.7 492 1 MOT3\_MOUSE  
42 57 15.7 492 1 MOT3\_RAT  
43 56.5 15.6 428 1 GBA1\_CANAL  
44 56.5 15.6 470 1 RHA\_RHIME  
45 56.5 15.6 487 1 DLTA\_STAXY

## ALIGNMENTS

### RESULT 1

VAL1\_TGMV STANDARD; PRT; 352 AA.

AC P03567;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE ALL protein.

GN ACl.

OS Tomato golden mosaic virus (TGMV).

OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

OX NCBI TaxID=10831;

RN [1]

RP SEQUENCE FROM N.A.

RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;

RT "Complete nucleotide sequence of the infectious cloned DNA components

of tomato golden mosaic virus: potential coding regions and regulatory

sequences.";

RL EMBO J. 3:2197-2205(1984).

CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.

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CC EMBL; K02029; -; NOT ANNOTATED CDS.

DR PIR; A04170; QCCVLI.

DR InterPro; IPR001191; Gemini\_All.

DR Pfam; PF00799; Gemini\_All; 1.

DR PRINTS; PR00227; GEMCOATALL.

DR ProDom; PD000736; Gemini\_All; 1.

KW ATP-binding. 223 230 ATP (POTENTIAL).

FT NP\_BIND 223 230

SQ SEQUENCE 352 AA; 40332 MW; C33C938E9644B4A4 CRC64;

Query Match

Best Local Similarity 98.3%; Score 356; DB 1; Length 352;

Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLVWGFQVAGRSARGCQTSNDAAALNASSKEALQIIRKIPKYLQFHNLSNL 60

DB 111 TLVWGFQVQGRSARGCQTSNDAAALNASSKEALQIIRKIPKYLQFHNLSNL 170

QY 61 DRIFDKTPEP 70

DB 171 DRIFDKTPEP 180

### RESULT 2

VAL1\_PYMV

ID VAL1\_PYMV STANDARD; PRT; 361 AA.

AC P27258;



```

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE All protein.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
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CC -----
DR EMBL; D00940; BAA0782.1; -
DR PIR; J00364; QCCVPT.
DR InterPro; IPR001191; Gemini_All1.
DR Pfam; PF00799; Gemini_All1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_All1; 1.
DR ATP-binding.
KW NP BIND. 222 229 ATP (POTENTIAL).
FT SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;
SQ
Query Match 70.7%; Score 256; DB 1; Length 361;
Best Local Similarity 69.6%; Pred. No. 3.3e-21;
Matches 48; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGQTSNDAAALNASSKEALQIIREKIPKYLFPQHNLNSNL 60
Db 110 TIWGLFQIDGSRGSGGQTSNDAAALNASSKEALQIIREKIPKYLFPQHNLNSNL 169
QY 61 DRIFDKTPE 69
Db 170 DRIFWKAPE 178

RESULT 3
VAL1_CLVK STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE All1 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RX Stanley J., Gay M.R.;
RA "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
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CC EMBL; J02057; -, NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_All1.
DR Pfam; PF00799; Gemini_All1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_All1; 1.
KW ATP-binding.
FT NP BIND. 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173E753EE92D69 CRC64;

Query Match 67.1%; Score 243; DB 1; Length 358;
Best Local Similarity 62.9%; Pred. No. 9.1e-20;
Matches 44; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGQTSNDAAALNASSKEALQIIREKIPKYLFPQHNLNSNL 60
Db 109 TVWQGFQIDGSRGSGGQTSNDAAALNASSKEALQIIREKIPKYLFPQHNLNSNL 169
QY 61 DRIFDKTPE 70
Db 169 DRIFQEPAP 178

RESULT 4
VAL1_CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE All1 protein (40.4 kDa protein).
GN AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain)."
RL Nucleic Acids Res. 18:197-198(1990).
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CC -----
DR EMBL; X17095; CAA34953.1; -
DR PIR; S07594; S07594.
DR InterPro; IPR001191; Gemini_All1.
DR Pfam; PF00799; Gemini_All1; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_All1; 1.
KW ATP-binding.
FT NP BIND. 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16BB0CB2D5E2C CRC64;

Query Match 67.1%; Score 243; DB 1; Length 358;
Best Local Similarity 62.9%; Pred. No. 9.1e-20;
Matches 44; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGGQTSNDAAALNASSKEALQIIREKIPKYLFPQHNLNSNL 60
Db 109 TVWQGFQIDGSRGSGGQTSNDAAALNASSKEALQIIREKIPKYLFPQHNLNSNL 168
QY 61 DRIFDKTPE 70
Db 169 DRIFQEPAP 178

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CC EMBL; Z25751; CAA81026.1; -  
DR PIR; S39211; S39211.  
DR InterPro; IPR001191; Gemini\_AL1.  
DR Pfam; PF00799; Gemini\_AL1; 1.  
DR PRINTS; PR00227; GEMCOATL1.  
DR ProDom; PD000736; Gemini\_AL1; 1.  
KW ATP-binding. 221 228 ATP (POTENTIAL).  
FT NP BIND 359 AA; 41065 MW; 2D170A51EF80A3EC CRC64;  
SQ SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3EC CRC64;  
  
Query Match 63.3%; Score 229; DB 1; Length 359;  
Best Local Similarity 60.9%; Pred. No. 3.3e-18;  
Matches 42; Conservative 9; Mismatches 18; Indels 0; Gaps 0;  
  
QY 2 LTVGFEQVAGSARGCGQTSNDAAAEALNASKEALQIIREKIPEKYLQFHNLSNLD 61  
DB 111 LEWGTFTQDGRSARGCGQTSNDAAAEALNASKEALQIIREKIPEKYLQFHNLSNLD 170  
QY 62 RIFDKTPEP 70  
DB 171 RVFQVPPAP 179  
  
RESULT 3  
VAL1 PHUV STANDARD; PRT; 349 AA.  
AC Q06923;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE AL1 protein.  
GN AL1.  
OS Pepper huasteco virus (PHV)  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=28349;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94015007; PubMed=8409944;  
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,  
RA Rivera-Bustamante R.F.;  
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and  
RT comparison with bipartite geminiviruses.";  
RL J. Gen. Virol. 74:2225-2231(1993).  
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.  
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CC  
DR EMBL; X70418; CAA49856.1; -  
DR PIR; JQ2300; JQ2300.  
DR PIR; S31875; S31875.  
DR InterPro; IPR001191; Gemini\_AL1.  
DR Pfam; PF00799; Gemini\_AL1; 1.  
DR PRINTS; PR00227; GEMCOATL1.  
DR ProDom; PD000736; Gemini\_AL1; 1.  
KW ATP-binding. 221 228 ATP (BY SIMILARITY).  
FT NP BIND 349 AA; 39722 MW; D5F4E76CD56370F4 CRC64;  
SQ SEQUENCE 349 AA; 39722 MW; D5F4E76CD56370F4 CRC64;  
  
Query Match 62.2%; Score 225; DB 1; Length 349;  
Best Local Similarity 60.0%; Pred. No. 9.1e-18;  
Matches 42; Conservative 13; Mismatches 13; Indels 0; Gaps 0;  
  
QY 1 TLVWGEFQVAGSARGCGQTSNDAAAEALNASKEALQIIREKIPEKYLQFHNLSNLD 60  
DB 110 TLVWGEFQDGRSARGCGQTSNDAAAEALNASKEALQIIREKIPEKYLQFHNLSNLD 169

61 DRIEDKTPPEP 70  
:|||||  
170 NRIFQTPPEP 179

ULT 8  
J1 VAL1 TYLCM STANDARD; PRT; 359 AA.  
P27260;  
01-AUG-1992 (Rel. 23, Created)  
01-AUG-1992 (Rel. 23, Last sequence update)  
15-SEP-2003 (Rel. 42, Last annotation update)  
Al1 protein (Cl protein).  
Cl.  
Tomato yellow leaf curl virus (strain Marmande) (TYLCV).  
Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
NCBI\_TaxID=10833;  
[1]  
P SEQUENCE FROM N.A.  
MEDLINE=92107660; PubMed=1840676;  
A Kheyr-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,  
A Gronenborn B.; leaf curl virus from Sardinia is a  
T whitefly-transmitted monopartite Geminivirus.;  
L Nucleic Acids Res. 19:6763-6769 (1991).  
C -|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.  
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C  
C EMBL; M10070; AAA46318.1; -;  
C InterPro; IPR001191; Gemini\_AL1.  
C Pfam; PF00799; Gemini\_AL1; 1.  
C PRINTS; PR00227; GEMCOATALL.  
C ProDom; PD000736; Gemini\_AL1; 1.  
C ATP-binding.  
C NP BIND 222 229 ATP (POTENTIAL).  
C SEQUENCE 353 AA; 40733 MW; 9717B4A07C93EFA7 CRC64;  
Query Match 61.3%; Score 222; DB 1; Length 359;  
Best Local Similarity 58.0%; Pred. No. 2e-17;  
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;  
QY 2 LVWGEFQVAGRSARGGCGTSDNDAALNASSKEALQIIREKIPKYLFOFHNLSNLD 61  
Db 111 LEWGTQIDRSARGGCGTSDNDAALNASSKEALQIIREKIPKYLFOFHNLSNLD 170  
QY 62 RIFDKTPPEP 70  
:|||||  
171 KVQVPPAP 179

RESULT 9  
VAL1 BGWV STANDARD; PRT; 353 AA.  
AC F05175;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE AL1 protein (40.2 kDa protein).  
GN AC1.  
OS Bean golden mosaic virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=10833;  
RN [1]

SEQUENCE FROM N.A.  
Howarth A.J., Caton J., Bossert M., Goodman R.M.;  
"Nucleotide sequence of bean golden mosaic virus and a model for gene  
regulation in geminiviruses";  
Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576 (1985).  
-|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.  
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C  
C EMBL; M10070; AAA46318.1; -;  
C InterPro; IPR001191; Gemini\_AL1.  
C Pfam; PF00799; Gemini\_AL1; 1.  
C PRINTS; PR00227; GEMCOATALL.  
C ProDom; PD000736; Gemini\_AL1; 1.  
C ATP-binding.  
C NP BIND 222 229 ATP (POTENTIAL).  
C SEQUENCE 353 AA; 40190 MW; 80FA77DF6029A34 CRC64;  
Query Match 60.8%; Score 220; DB 1; Length 353;  
Best Local Similarity 60.0%; Pred. No. 3.3e-17;  
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;  
QY 1 TLVWGEFQVAGRSARGGCGTSDNDAALNASSKEALQIIREKIPKYLFOFHNLSNLD 60  
Db 110 TIWGGQFQVDSARGGCGTSDNDAALNASSKEALQIIREKIPKYLFOFHNLSNLD 169  
QY 61 DRIEDKTPPEP 70  
:|||||  
170 ERIFQVPPAP 179

RESULT 10  
VAL1 ABMVV STANDARD; PRT; 355 AA.  
AC P21947;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE AL1 protein.  
GN AC1.  
OS Abutilon mosaic virus (isolate West India).  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=10816;  
RN [1]  
RP SEQUENCE FROM N.A.  
MEDLINE=91020984; PubMed=2219703;  
RA Frischmuth T., Zimmat G., Jeske H.;  
"The nucleotide sequence of abutilon mosaic virus reveals prokaryotic  
as well as eukaryotic features";  
Virology 178:461-468 (1990).  
-|- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.  
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C  
C EMBL; X15983; -; NOT ANNOTATED\_CDS.  
C PIR; A36214; QOCVW1.  
C InterPro; IPR001191; Gemini\_AL1.  
C Pfam; PF00799; Gemini\_AL1; 1.  
C PRINTS; PR00227; GEMCOATALL.  
C ProDom; PD000736; Gemini\_AL1; 1.  
C ATP-binding.  
KW

```

FT NP BIND 221 228 ATP (POTENTIAL)
SQ SEQUENCE 355 AA; 40257 MW; 16A2CAGA63251E95 CRC64;

Query Match 60.5%; Score 219; DB 1; Length 355;
Best Local Similarity 58.6%; Pred. No. 4.3e-17;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVGEFQVAGRGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSL 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TAEGEFQIDGRSGRGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSL 169
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DRIFDKTPEP 70
   :|||:|||||:
Db 170 ERIFAKAPEP 179
   :|||:|||||:

RESULT 11
VAL1 BCTV STANDARD; PRT; 358 AA.
AC P14951;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 protein (40.8 kDa protein).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
   beet curly top virus."
RL EMBO J. 5:1761-1767(1986).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; L14460; AAC32414.1; -
DR PIR; JQ1870; JQ1870.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALI.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
RN NP BIND 222 229 ATP (BY SIMILARITY).
RP SEQUENCE 358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
   beet curly top virus."
RL EMBO J. 5:1761-1767(1986).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; X04144; -; NOT ANNOTATED CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATALI.
DR ProDom; PD000736; Gemini_AL1; 1.
KW ATP-binding.
RN NP BIND 222 229 ATP (POTENTIAL).
RP SEQUENCE 358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
   beet curly top virus."
RL EMBO J. 5:1761-1767(1986).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
Query Match 59.7%; Score 216; DB 1; Length 358;
Best Local Similarity 55.7%; Pred. No. 9.5e-17;
Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVGEFQVAGRGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSL 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TIEGFEQIDGRSGRGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSL 169
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DRIFDKTPEP 70
   :|||:|||||:
Db 170 QKIFORPPDP 179
   :|||:|||||:

RESULT 12
VAL1 TMOV STANDARD; PRT; 361 AA.
AC Q0657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein.

Query Match 59.7%; Score 216; DB 1; Length 358;
Best Local Similarity 55.7%; Pred. No. 9.5e-17;
Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVGEFQVAGRGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSL 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TIEGFEQIDGRSGRGCGQTSNDAAAEALNASSKEEALQIIRKIPKYLQFPHNLNSL 169
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DRIFDKTPEP 70
   :|||:|||||:
Db 170 QKIFORPPDP 179
   :|||:|||||:

RESULT 13
VAL1 TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 protein (C1 protein).
GN C1
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RP SEQUENCE FROM N.A.
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
   with a single genomic component."
RL Virology 185:151-161(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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DR EMBL; X15656; CAA33688.1; -.
DR PIR; D40779; QOCVCI.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1.1.
DR ATP-binding. 219 226 ATP (POTENTIAL).
FW NP_BIND 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match 57.2%; Score 207; DB 1; Length 357;
Best Local Similarity 65.6%; Pred. No. 9.5e-16;
Matches 40; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 4 WGEFQVAGRSAGCGQTNDAAAEALNASSKEALQIREKIPEKYLFOFHNLSNLDRI 63
DB 111 FGVSQIDGRSAGCGQTSANDAYAEALNSGSKSEALNLIKERAPKDYILQFHNLSNLDRI 170

QY 64 F 64
DB 171 F 171

RESULT 14
VAL1_SLVC STANDARD; PRT; 347 AA.
ID VAL1_SLVC
AC Q90XB3; Q90XC8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Oligodendrocyte transcription factor 2.
GN Olig2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21453760; PubMed=11567617;
RA Zhou Q., Choi G., Anderson D.J.;
RT "The bHLH transcription factor Olig2 promotes oligodendrocyte
RT differentiation in collaboration with NKX2.2."
RL Neuron 31:791-807(2001).
RN [2]
RP SEQUENCE OF 99-161 FROM N.A.
RX MEDLINE=21453759; PubMed=11567616;
RA Novitsch B.G., Chen A.I., Jessell T.M.;
RT "Coordinate regulation of motor neuron subtype identity and
RT pan-neuronal properties by the bHLH repressor Olig2."
RL Neuron 31:773-789(2001).
CC -!- FUNCTION: Required for oligodendrocyte and motor neuron
CC specification in the spinal cord (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
CC
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CC
CC EMBL; AF411041; AAL11883.1; -.
CC EMBL; AF405699; AAL02428.1; -.
CC InterPro; IPR001092; HLH_basic.
CC Pfam; PF00010; HLH; 1.
CC SMART; SM00353; HLH; 1.
CC PROSITE; PS00038; HLH 1; 1.
CC PROSITE; PS50888; HLH 2; 1.
CC Transcription regulation; DNA-binding; Nuclear protein.
FT DNA_BIND 107 118
FT DOMAIN 119 160 BASIC DOMAIN.
FT DOMAIN 24 42 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT DOMAIN 45 92 GLY-RICH.
FT DOMAIN 55 92 SER-RICH.
SQ SEQUENCE 298 AA; 30319 MW; 5790A79F2764F5D8 CRC64;

Query Match 18.1%; Score 65.5; DB 1; Length 298;
Best Local Similarity 32.2%; Pred. No. 5;
Matches 19; Conservative 13; Mismatches 20; Indels 7; Gaps 1;

QY 17 GCOTSDNDAAEALNASSK-----EALQIREKIPEKYLFOFHNLSNLDRI 68
DB 76 GFKSSSSASSASSASSKDKQKQTEPELQURLKINSRKRMEDLNAMDGLREVMP 134

Search completed: December 23, 2003, 08:57:40
Job time : 5.77778 secs

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RESULT 2
Q9E000
ID Q9E000 PRELIMINARY; PRT; 352 AA.
AC Q9E000;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Replication-associated protein.
GN AC1.
OS Tomato rugose mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=134599;
RN [1]
RP SEQUENCE FROM N.A.
RA Fernandes J.J., Fontes E.P.B., Brommonschenkel S.H., Carvalho M.G.,
Zambolim E.M., Zerbini F.M.;
RT "Molecular Cloning and Characterization of Tomato rugose mosaic virus
(TMV), a Begomovirus Isolated from Tomatoes at Triangulo Mineiro,
Minas Gerais, Brazil.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF291705; AAG15546.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 352 AA; 40012 MW; 47CD55838E24D613 CRC64;

Query Match 84.3%; Score 305; DB 12; Length 352;
Best Local Similarity 81.4%; Pred. No. 9e-27; Indels 0; Gaps 0;
Matches 57; Conservative 7; Mismatches 6;

QY 1 TLVWGFQVAGRSARGCGCQTNDAAAEALNASSKEALQIIRKPKYLFQFHNLSNL 60
Db 111 TLWGFQVAGRSARGCGCQTNDAAAEALNASSKEALQIIRKPKYLFQFHNLSNL 170

QY 61 DRIFDKTPEP 70
Db 171 DRIFAKAPEP 180

RESULT 3
Q8QPV3
ID Q8QPV3 PRELIMINARY; PRT; 232 AA.
AC Q8QPV3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Tomato chlorotic vein virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172390;
RN [1]
RP SEQUENCE FROM N.A.
RA Ribeiro S.G., Ambrozovic L.P., de Avila A.C., Calegario R.F.,
Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049205; AAL82824.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 232
SQ SEQUENCE 232 AA; 26319 MW; 254CA5D040D35DDA CRC64;

Query Match 82.0%; Score 297; DB 12; Length 232;
Best Local Similarity 80.0%; Pred. No. 4.6e-26;
Matches 56; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLVWGFQVAGRSARGCGCQTNDAAAEALNASSKEALQIIRKPKYLFQFHNLSNL 60
Db 111 TLWGFQVAGRSARGCGCQTNDAAAEALNASSKEALQIIRKPKYLFQFHNLSNL 170

RESULT 4
Q9WHF6
ID Q9WHF6 PRELIMINARY; PRT; 226 AA.
AC Q9WHF6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Replication-associated protein (Fragment).
GN REP.
OS Tomato mild mottle geminivirus.
OC Viruses; ssDNA viruses; Geminiviridae; unclassified Geminiviridae.
OX NCBI_TaxID=92943;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=HN96-H5kw;
RA Nakha M.K., Mejia L., Ramirez P., Karkashian J.P., Doyle M.M.,
Maxwell D.P.;
RT "Molecular characterization and DNA-based detection methods for
vegetable-infecting geminiviruses in Central America.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131071; AAD3471.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 226
SQ SEQUENCE 226 AA; 25941 MW; 2EA4116712871A23 CRC64;

Query Match 79.6%; Score 288; DB 12; Length 226;
Best Local Similarity 75.7%; Pred. No. 4.8e-25;
Matches 53; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVAGRSARGCGCQTNDAAAEALNASSKEALQIIRKPKYLFQFHNLSNL 60
Db 111 TLWGFQVAGRSARGCGCQTNDAAAEALNASSKEALQIIRKPKYLFQFHNLSNL 170

QY 61 DRIFDKTPEP 70
Db 171 DRIFAKAPEP 180

RESULT 5
Q09727
ID Q09727 PRELIMINARY; PRT; 226 AA.
AC Q09727;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN REP.
OS Leonurus mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=58177;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=LeMV- Brazil 1;
RA Faria J.C., Maxwell D.P.;
RT "Variability in geminivirus associated with Phaseolus vulgaris in
Brazil.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U92532; AAB51157.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 226
SQ SEQUENCE 226 AA; 25941 MW; 2EA4116712871A23 CRC64;

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SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;
Query Match 79.6%; Score 288; DB 12; Length 226;
Best Local Similarity 80.0%; Pred. No. 4.8e-25;
Matches 56; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
DB 111 TVWGEFQVDRSGRGQQTIVNDAAAEALNAPDKRTALQIIREKIPEKYLFOFHNLSNL 170

QY 61 DRIPDKTPEP 70
DB 171 DRIFAKAPEP 180

RESULT 6
Q67574 PRELIMINARY; PRT; 361 AA.
AC Q67574;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative replicative protein.
GN All.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration."
RL Phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RT "Differentiation of bean-infecting geminiviruses by nucleic acid
RT hybridization probes and aspects of bean golden mosaic in Brazil."
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus."
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M86866; AAA46312.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 79.0%; Score 286; DB 12; Length 361;
Best Local Similarity 79.1%; Pred. No. 1.4e-24;
Matches 53; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 4 WGEFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 63
DB 113 WGHFQVDRSGRGQQTANDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 172

QY 64 FDKTPEP 70
DB 173 FTKAPDP 179

RESULT 7
Q9QDB1 PRELIMINARY; PRT; 225 AA.
AC Q9QDB1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Replication associated protein (fragment).
GN REP.
OS Cowpea golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RP SEQUENCE FROM N.A.
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RT Brazil."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF198708; AAF06318.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
FT NON TER 225
SQ SEQUENCE 225 AA; 25766 MW; 1089CB6BD8D15B5D CRC64;

Query Match 78.5%; Score 284; DB 12; Length 225;
Best Local Similarity 79.1%; Pred. No. 1.4e-24;
Matches 53; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 4 WGEFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 63
DB 113 WGHFQVDRSGRGQQTINDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 172

QY 64 FDKTPEP 70
DB 173 FTKAPDP 179

RESULT 8
Q9ELT8 PRELIMINARY; PRT; 314 AA.
AC Q9ELT8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Replication association protein.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States."
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF298227; AAG01006.1; -.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1; I.
DR PRINTS; PR00227; GEMCOATALL.
DR ProDom; PD000736; Gemini_AL1; 1.
SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 78.5%; Score 284; DB 12; Length 314;
Best Local Similarity 82.4%; Pred. No. 2e-24;
Matches 56; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGFQVAGRSARGCGQTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 60
DB 110 TITWGEFQVDRSGRGQQTANDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLSNL 169

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QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 9
Q9Q55 PRELIMINARY; PRT; 364 AA.
AC Q9Q55;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Replication initiation protein AC1.
GN AC1.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT "Cloning of a DNA-A-like genomic component of sweet potato leaf curl
RT virus; nucleotide sequence and phylogenetic relationships.";
RL Mol. Plant Pathol. On-Line 0:0-0(1999).
DR EMBL; AF104036; AAD4173.1; -.
DR InterPro; IPR001191; Gemin_A11.
DR Pfam; PF00799; Gemin_A11; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR ProDom; PD000736; Gemin_A11; 1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 78.5%; Score 284; DB 12; Length 364;
Best Local Similarity 82.4%; Pred. No. 2.4e-24;
Matches 56; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGFQVAGRSARGCGCOTSDNAAAEALNASSKEEALQIIRKIPKYLFOFHNLSNL 60
Db 110 TIWGFQVAGRSARGCGCOTSDNAAAEALNASSKEEALQIIRKIPKYLFOFHNLSNL 169

QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

RESULT 10
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rep protein (Fragment).
GN AC1.
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA SFRATN=Jamaica;
RC SFRATN=Jamaica;
RA Roye M.E., McLaughlin W.A., Nakhla N.K., Maxwell D.P.;
RT "Genetic Diversity among geminiviruses associated with the weed
RT species Sida spp, Macroptilium lathyroides, and Wissadula amplissima
RT from Jamaica.";
RL Plant Dis. 81:1251-1258(1997).
DR EMBL; U67926; AAB97865.1; -.
DR InterPro; IPR001191; Gemin_A11.
DR Pfam; PF00799; Gemin_A11; 1.
DR PRINTS; PR00227; GEMCOATL1.

QY 61 DRIFDKTP 68
Db 170 DRIFSPPP 177

Query Match 76.5%; Score 277; DB 12; Length 235;
Best Local Similarity 76.1%; Pred. No. 9.2e-24;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 4 WGEFQVAGRSARGCGCOTSDNAAAEALNASSKEEALQIIRKIPKYLFOFHNLSNL 63
Db 113 WGIFQIDGRSARGCGCOTSDNAAAEALNASSKEEALQIIRKIPKYLFOFHNLSNL 172

QY 64 DRIFDKTP 70
Db 173 FTKAPDP 179

RESULT 12
Q8JLY3 PRELIMINARY; PRT; 208 AA.
AC Q8JLY3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;

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RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY126611; AM95995.1; -
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATL1.
DR ProDom: PD000736; Gemini_AL1; 1.
FT NON_TER 208
SQ SEQUENCE 208 AA; 23667 MW; 51211D58PAD690A6 CRC64;

Query Match 76.2%; Score 276; DB 12; Length 208;
Best Local Similarity 72.9%; Pred. No. 1e-23;
Matches 51; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TLVWGFQVAGRSARGCGCQTSNDAAAEALNASSKEALQIIRKIPKYLFOYHNLNSNL 60
   |||||
Db 110 TIWGLVFQIDGRSARGGQQTSDNDAAEALNASSKEALQIIRKIPKYLFOYHNLSSNL 169

Qy 61 DRIFDKTPEP 70
   |||||
Db 170 DRIFMKAPKP 179

RESULT 13
Q8JLY5 PRELIMINARY; PRT; 289 AA.
AC Q8JLY5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbino C., Polston J.E., Patte C.P., Caruana M.-L.;
RT "Characterization and genetic diversity of PYMV from the Caribbean.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY126610; AM95993.1; -
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATL1.
DR ProDom: PD000736; Gemini_AL1; 1.
FT NON_TER 289
SQ SEQUENCE 289 AA; 32971 MW; 4ECF52F4C69C6764 CRC64;

Query Match 76.2%; Score 276; DB 12; Length 289;
Best Local Similarity 72.9%; Pred. No. 1.5e-23;
Matches 51; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TLVWGFQVAGRSARGCGCQTSNDAAAEALNASSKEALQIIRKIPKYLFOYHNLNSNL 60
   |||||
Db 110 TIWGLVFQIDGRSARGGQQTSDNDAAEALNASSKEALQIIRKIPKYLFOYHNLSSNL 169

Qy 61 DRIFDKTPEP 70
   |||||
Db 170 DRIFMKAPKP 179

RESULT 14
P88975 PRELIMINARY; PRT; 149 AA.
AC P88975;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication-associated protein (Fragment).
GN AC1.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;

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RN SEQUENCE FROM N.A.
RP STRAIN=Jamaican;
RA Roye M.E.; Biochemistry, University of the West Indies, Jamaica.
RL Thesis (1996); AAB36919.1; -.
DR EMBL: U75278; AAB36919.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATL1.
DR ProDom: PD000736; Gemini_AL1; 1.
FT NON_TER 149
SQ SEQUENCE 149 AA; 16785 MW; E4CF5EBD4C9CD508 CRC64;

Query Match 75.4%; Score 273; DB 12; Length 149;
Best Local Similarity 71.4%; Pred. No. 1.5e-23;
Matches 50; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TLVWGFQVAGRSARGCGCQTSNDAAAEALNASSKEALQIIRKIPKYLFOYHNLNSNL 60
   |||||
Db 52 TIWGLVFQIDGRSARGGQQTSDNDAAEALNASSKEALQIIRKIPKYLFOYHNLSSNL 111

Qy 61 DRIFDKTPEP 70
   |||||
Db 112 DRIFMKDPEP 121

RESULT 15
Q9YLA4 PRELIMINARY; PRT; 233 AA.
AC Q9YLA4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Replication associated protein (Fragment).
GN REP.
OS Macroptilium golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
RN [1]
RP SEQUENCE FROM N.A.
RA Roye M.E.;
RT "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Jamaica strain 1;
RA Roye M.E., McLaughlin W.A., Maxwell D.P.;
RT "Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF098940; AADI7850.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATL1.
DR ProDom: PD000736; Gemini_AL1; 1.
FT NON_TER 233
SQ SEQUENCE 233 AA; 26356 MW; AA490AF4D2166A02 CRC64;

Query Match 75.4%; Score 273; DB 12; Length 233;
Best Local Similarity 71.4%; Pred. No. 2.6e-23;
Matches 50; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TLVWGFQVAGRSARGCGCQTSNDAAAEALNASSKEALQIIRKIPKYLFOYHNLNSNL 60
   |||||
Db 110 TIWGLVFQIDGRSARGGQQTSDNDAAEALNASSKEALQIIRKIPKYLFOYHNLSSNL 169

Qy 61 DRIFDKTPEP 70
   |||||
Db 170 DRIFMKDPEP 179

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Job time : 25.3333 secs

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